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Result
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Maximum Match 100%
Listing first 45 summaries
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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WS-11-187-188-8-309
WS-11-186-284-102
WS-11-750-185-47425
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Sequence 55754, A
Sequence 55754, A
Sequence 531, App
Sequence 86, Appl
Sequence 199, Appl
Sequence 209, Appl
Sequence 209, Appl
Sequence 40243, A
Sequence 61642, A
Sequence 211, Appl
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| .0 4339 6 .0 161874 7 .9 189252 7 .9 189253 7 .9 18557 6 .9 3657 6 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 7 .9 16450 6 .9 1742 6 .9 1742 6 .9 1742 6 .9 1746 6 .9 1746 6 6 .9 1746 6 6 .9 174 | .0 4339 6 US-10-909-125-801 Sequence 2356 6 US-10-821-234-815 Sequence 0 161874 7 US-11-121-086-75 Sequence 0 161874 7 US-11-121-086-75 Sequence 19184000 7 US-11-121-086-37 Sequence 1918993 7 US-11-121-086-74 Sequence 1918993 7 US-11-121-086-78 Sequence 1918993 7 US-11-121-086-78 Sequence 1918993 7 US-11-121-086-78 Sequence 1918993 7 US-10-750-185-62187 Sequence 1918993 7 US-10-750-185-63154 Sequence 1918993 7 US-10-750-185-63154 Sequence 1918993 7 US-11-0750-185-63154 Sequence 1918993 7 US-11-121-086-73 Sequence 1918993 7 US-11-121-086-73 Sequence 1918993 7 US-11-121-086-73 Sequence 1918993 7 US-10-750-185-62008 Sequence 1918993 7 US-10-750-185-62008 Sequence 1918993 Sequence 19189993 Sequence 1918993 Sequence | 35                  | <b>3</b> 5          | 35                  | 35.2              | 35.2            | 35.2                | 35.2                | 35.4   | 35.4 | 35.4            | 35.6 | 35.6                | 35.6                | 35.6                | 35.8   | 35.8   | 35.8             | 35.8 | 36               | 36                | 36.2              |   |
| <b>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</b>   | 6 US-10-909-125-801 Sequence 6 US-10-821-234-815 Sequence 7 US-11-121-086-75 Sequence 7 US-11-121-086-75 Sequence 7 US-11-121-086-37 Sequence 9 US-11-121-086-74 Sequence 9 US-11-121-086-78 Sequence 10 US-11-121-086-78 Sequence 10 US-10-750-185-62887 Sequence 10 US-10-750-185-63154 Sequence 10 US-10-750-185-43919 Sequence 10 US-11-179-411-5 Sequence 10 US-11-179-411-5 Sequence 10 US-11-179-411-5 Sequence 10 US-10-750-185-62008 Sequence 10 US-10-750-185-6391 Sequence 10 US-10-750-185-64507 Sequence 10 US-10-750-185-64507 Sequence 10 US-10-750-185-54507 Sequence  | 2.9                 | 2.9                 | 2.9                 | 2.9               | 2.9             | 2.9                 | 2.9                 | 2.9    | 2.9  | 2.9             |      |                     |                     | 2.9                 | 2.9    | 2.9    | 2.9              | 2.9  | 3.0              | 3.0               | 3.0               |   |
|  | US-10-909-125-801  US-10-909-125-801  Sequence US-11-121-086-75  Sequence US-11-121-086-37  US-11-121-086-37  US-11-121-086-37  US-11-121-086-37  US-11-121-086-37  US-11-121-086-38  US-11-121-086-39  US-11-121-086-39  US-11-091-68-3154  US-10-750-185-62887  US-10-750-185-63154  US-11-121-086-31  US-11-121-086-37  US- | 1468                | 1267                | 959                 | 43948             | 21777           | 1720                | 742                 | 164527 | 1608 | 958             | 6450 | 3657                | 1619                | 794                 | 189993 | 189252 | 184000           | 1073 | 161874           | 2356              | 4339              |   |
| US-10-99-125-801 US-10-821-234-815 US-11-121-086-75 US-11-121-086-75 US-11-121-086-37 US-11-121-086-54 US-11-121-086-78 US-11-121-086-78 US-11-750-185-62887 US-10-750-185-63154 US-10-750-185-63154 US-10-750-185-6208 US-10-750-185-24686 US-10-750-185-24686 US-10-750-185-46342 US-10-750-185-62008 US-11-027-964-2 US-10-750-185-620341 US-10-750-185-63341 US-10-750-185-63341 US-10-750-185-63341 US-10-750-185-63341   | 10-909-125-801 10-821-234-815 10-821-234-815 11-121-086-75 11-121-086-37 11-121-086-37 11-121-086-37 11-121-086-78 11-121-086-78 11-121-086-78 11-121-086-78 11-121-086-79 11-750-185-62887 11-750-185-43919 11-091-668-3 11-091-6 | σ                   | σ                   | 6                   | 0                 | 7               | σ                   | σ                   | 7      | 6    | 7               | 7    | 6                   | σ                   | σ                   | 7      | 7      | 7                | 7    | 7                | 6                 | σ                 | • |
|  |  | US-10-750-185-57297 | US-10-750-185-54507 | US-10-750-185-60341 | US-10-949-720-393 | US-11-027-964-2 | US-10-750-185-43422 | US-10-750-185-62008 | Ξ      | 5    | US-11-179-411-5 | Ξ    | US-10-750-185-43919 | US-10-750-185-63154 | US-10-750-185-62887 | 두      | 11-121 | US-11-121-086-37 | 5    | US-11-121-086-75 | US-10-821-234-815 | US-10-909-125-801 |   |

## ALIGNMENTS

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US-11-117-187-203

Sequence 203, Application US/1117187

Publication No. US20050266560A1

GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER,
APPLICANT: COPENHAVER,
APPLICANT: COPENHAVER,
APPLICANT: COPENHAVER,
CURRENT APPLICATION NUMBER: US/11/117,187

CURRENT APPLICATION NUMBER: US/09/531,120

PRIOR APPLICATION NUMBER: US/09/531,120

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/125,219

PRIOR APPLICATION NUMBER: 60/125,219

PRIOR FILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 212

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 203

TYPE: DNA
ORGANISM: Arabidonsis thaliana
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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US-10-750-185-55754/c
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; ORGANISM: Bovine
US-10-750-185-25798
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MMI GENONICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-750-185-25798/c
                                                                                                                                                                                                                                                                                                                        Sequence 55754, Application US/10750185 Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1110-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: Patentin version 3.1

LENGTH: 1711
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Best Local
SOFTWARE: PatentIN version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25798, Application US/10750185 Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENEELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1003 ATAATTTCCCTTTTCAAATTAAATTAATCTGCAATATATTAGTCATTGTCTCAAATGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1063 TTTCTGTAGCCTCAATATACAGTATTGAGAGAAGGAGATATACAATAAAAATTTTTAAAA 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                  823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 TTTGTTTCCTCTCGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATTAATC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAGCACATITACAAGGGCTGATCTTAGCCTTTATATTTACAATAAAGAAAATAAACCA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCTGAGAAAACTGATGTTGGTAACTTGATTTAATAATATCAAACTGGGTTAAAATAAA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAAAGTCTGTAGAAAAGGAAGTATAATTTTTTAAAACCATAACAATGAGAAAAAAGCA
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                                                                                                                                                                                                                ROSENFELD, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 0.073;
0; Mismatches 161;
                                                                                                                                       BOVINE
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US-10-750-185-54114/c
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Best Local Similarity
Matches 140; Conserv
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LENGTH: 1625
1514 ATAAAATAAATACTTGTAAGCAACAAAACAAAAACCACAAAGCTTATGTATTTTATTT
                                                         432 ААААТААЛААААТGTGCATAACTTAAAAAAAAAAACCAAATACCAACAAGACTTTACTT
                                                                                                                                                               372 ACATGTGAGTGCTGAGAAAACTGATGTTGGTAACTTGATTTAATAATATCAAACTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 TAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTGGTAACTTGATTTAATAATATC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 GAGAATTGCAAATGAATAGGCACAAAGTACATAAAATTTCAAACTCAGATAATTATTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 CTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 ACCT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 GAAATAAGAGATTATCTGATTATCTGATGTATCCAACCATATTATAGTTTATATTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 GAGAATTATTTGAAGGTCTGTATTCTACATAGGCAGAAGGTTGTCTCCAAGAAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 TGAAGGAAAAGGTGTATGTTTGTTTCCTCTCGACATACTTCACTCAAATATCTATTGTTA
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                                                                                                                      AAAATTGATTGCATAGAATAATGATGCTGTTAACATTTTTCTATGGTCTTAGAATTTGAT
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Pred. No. 0.12;
0; Mismatches 164; Indels
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RESULT 5 US-10-131-826A-533

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                                                                                                                                        Best Loc
Matches
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LENGTH: 496
                                                                                                                                                                         Query Match
                                                                                                                                                                                                          OTHER INFORMATION: unknown base -10-131-826A-533
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                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                              OCATION: 396
                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/059263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/059184 FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/059115
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/056974 FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/059122
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/059588
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/059117
328 CCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAG 387
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                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumas,Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beresini, Maureen
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d, Steven
                                                                                                                                                       3.2%;
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                                                                                                                                    Score 39.4; DB Pred. No. 0.24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   See File Wrapper or PALM
                                                                                                                                                                       DB 6;
                                                                                                                                      73;
                                                                                                                                                                       Length 496;
                                                                                                                                      Indels
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                                                                                                                                   Gaps
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US-11-117-187-199/c
; Sequence 199, Application US/11117187; Publication No. US20050266560A1; GENERAL INFORWATION:
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; ORGANISM: Arabidopsis thaliana US-11-117-187-199
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 116; Conserv
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                                                                                                                                                                                            APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS
FILE REFERENCE: ARCD: 309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
                                                                                                                           PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/125,219 PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                 APPLICANT: PREUSS, DAPHNE APPLICANT: COPENHAVER, G
                                         TYPE: DNA
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ORGANISM: Homo sapiens
                                                              JENGTH: 101786
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Pred. No. 6.7;
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Sequence 209, Application US/1117187

Publication No. US20050266560A1

GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187

CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR APPLICATION UNMBER: US/09/531,120
PR
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US-11-117-187-209
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US-11-121-086-49
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
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Best Local :
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Best Local
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91; Conservative
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Pred. No. 6.8;
0; Mismatches 87;
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 54249
LENGTH: 789
TYPE: DNA
ORGANISM: BOVINE 19866881847788
US-10-750-185-54249
RESULT 11
US-10-750-185-49243
; Sequence 49243, Application US/10750185
; Publication No. US20050260603A1
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US-10-750-185-54249
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-209
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Best Local Similarity
Matches 113; Conserv
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MMI GENOMICS, I. APPLICANT: DeNISE, Sue K. APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                            Y Match 3.1%;
Local Similarity 52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201773 AAGTTCAAATACAAAATTTATTTAATTTAAACAAAAAACGTTTAGTAAGAATAATATT 201829
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                                                                                                                                                                             269 GACCAATAGCCCAACAAATTCACCTAGATTGAATATTGAGAACAAAAAGCTTACACTGAA
                                                                                                                                                                                                               586 TCCTAAAAGAACAGAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTC
                                                                                                                                                                                                                                                209 TAGCAAATÁCATTAGCAATGAAAAATATCATTGAAGAAAACCCTATAGATCTATTTCTAT
                                                                                                                                                                                                                                                                                  526 TAGCCTTTATATTTACAATAAAGAAATAAACCAAGGTCCCGATATAGCTGTAATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AGTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTGGTAACTTGA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 TATCTATTGTTACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTAT 349
                                                                                                              AGGGGACATATCGTACACAAAAATAAACAGGAGAAACTGCC
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                                                                                                                                                                                                                                                                                                                             Conservative
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nilarity 47.7%;
Conservative (
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                                                                                                                                                                                                                                                                                                                         Score 37.8; DB Pred. No. 0.86; O; Mismatches
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GENERAL INFORMATION:

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US-10-750-185-61642; Sequence 61642, Application US/10750185; Publication No. US20050260603A1
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                                                                                                                                                                                                                                                                                               ; ORGANISM: Bovine US-10-750-185-61642
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; ORGANISM: Bovine
US-10-750-185-49243
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 61642
LENGTH: 3631
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                                                                                                                                                   Matches 105;
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Best Local Similarity 50.8%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MMI GENOMICS, II
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, Dav
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 988
       2102
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                                              559 AAGGTCCCGATATAGCTGTAATTTTATTCCTAAAAGAACAGAAACTTTCACTATGCT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 GAAAAGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTACAATAAAGAAAATAAACC 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     655 TAGGATGTTAAGTATCTTAACTTTTTAACAGTACATATTAGAAAGTTGCTTTCTACT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSENFELD, David
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                                                                                                                                                   Conservative
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                                                                                                                                       Score 37.8; DB 6;
Pred. No. 2;
0; Mismatches 112;
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US-11-117-187-211/c
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Sequence 211, Application US/11117187 Publication No. US20050266560A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3381, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
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SEQ ID NO 3381
LENGTH: 4071
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CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 TTGTTTCCTCTCGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATTAATCA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129;
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                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGAGAAAACTGATGTTGGTAACTTGATTTAATAATATCAAACTGGGTTAAAAATAAAA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACACTGCATAGCAATATAAACATTTTTCATATACTATGGTGTGCCCGAATAGTGATAT 1499
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45.9%; Pred. No. 2.1;
ative 0; Mismatches
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APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
ITTLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28

PRIOR APPLICATION NUMBER: US/09/531,120

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APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
ITILE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 1909-03-18
PRIOR FILING DATE: 1999-03-18
INUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 211
LENGTH: 1082144
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-11-117-187-211
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US-11-117-187-211
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; ORGANISM: Arabidopsis thaliana
US-11-117-187-211
                                                                                                                                                                                                                                                                                              Query Match 3.1%; Score 37.6; DB 7; Length 1082144; Best Local Similarity 48.6%; Pred. No. 50; Matches 103; Conservative 0; Mismatches 109; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 211, Application US/11117187 Publication No. US20050266560A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.1%;
Best Local Similarity 50.3%;
Matches 93; Conservative
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Best Local :
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SEQ ID NO 211
LENGTH: 1082144
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PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
                                                       556880 ATATGTAAAATAATTATGTCCCATATTTAAATCAAAAGGTGTATTTTAGTAAAATCA 556939
                                                                                                                                     556820 GATATGAAATTATATTTTTTTTTACACTCGCATATTTTAGGCGGGCATTACCTAGTTTTT
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594 GAACAGAAACTTTCACTATGCTTTAAAATTAA 625
                                                                                534 ATATTTACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCTAAAA 593
                                                                                                                                                                         474 ACCAACAAGACTTTACTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTTT 533
                                                                                                                                                                                                                                                        414 АТАЛТАТСАЛАСТӨӨӨТТАЛАЛТАЛАЛАЛАЛАЛТӨГӨСАТАЛСТТАЛАЛАЛАЛАЛАЛАГ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 TAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 ACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATTAATCAGGCCAAACCACTT 333
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Pred. No. 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
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Db 556940 AAACTAAATTAAAAAATTGAGAGAAAAAGAA 556971

Search completed: December 12, 2005, 15:45:07 Job time : 249 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1: gb_ba:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No  |              | Query Match 99.9 65.0 65.0 20.0 119.6 119.5 119. | Query Query Query Page 128046 99.9 228046 65.0 228774 65.0 326933 20.0 191377 19.6 183215 19.5 240825 19.5 240825 19.5 240825 19.5 2424 11.6 221218 11.6 221218 | 114<br>114<br>114 | AC1129567<br>AC114044<br>AC11329667<br>AC1132966<br>AC018398<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC09109<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC0910<br>AC |
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| ი ი<br>ი თ | 239          | 19.6   | 183215<br>240825  | 6                 | AC091099<br>AX087869   |
| c 7        | 238<br>237.4 | 19.5<br>19.5   | 240825<br>6714  | დით               | AX523960<br>AY563557   |
| . 9        | 236.8        | 19.4   | 2471  | φ                 | BC027216   |
| 2 10       | 213          | 17.5   | 2424  | . 6               | AF004326   |
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| c 16       | 139.4        | 11.4   | 2846  | თ                 | AX458642   |
| c 17       | n.           | 4.8  | 2000  | თ                 | AX655393   |
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|-------------------|----------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|
| 5                 | 14       | 13                | 42                | 41                | 40                 | 39                 | 38                 | 37                 | 36                 | 35                 | 34                 | ü                  | 32                 | 31                 | 30                 | 29                 | 28                 | 27                 | 26                 | 25                 | 24                 | 23                 | 22                | 21                 | 20                | 19                 |
| 51.6              | 51.6     | 51.6              | 51.6              | 51.6              | 51.6               | 51.8               | 52                 | 52.2               | 52.2               | 52.4               | 52.6               | 52.8               | 53                 | 53                 | 53                 | 53.2               | 53.4               | 53.4               | 53.8               | 53.8               | 54                 | 54.4               | 54.4              | 54.6               | 55                | 55.2               |
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| 6523              | 6523     | 6523              | 6523              | 6523              | 2606               | 1522               | 226607             | 285836             | 166384             | 182871             | 1084               | 236582             | 237303             | 159184             | 125958             | 231489             | 1084               | 1084               | 110000             | 110000             | 176966             | 110000             | 15698             | 163149             | 10710             | 205066             |
| σ                 | σ        | σ                 | თ                 | σ                 | 15                 | N                  | 14                 | 14                 | U                  | N                  | N                  | 14                 | 14                 | 14                 | N                  | 14                 | N                  | N                  | N                  | N                  | ហ                  | 14                 | 0                 | 14                 | თ                 | 14                 |
| AX767564          | AX767488 | AX344713          | CQ807186          | CQ806912          | YSCMTCG07          | AY701231           | CR847902           | AC128556           | BX294132           | AC117176           | AB101024           | CR388102           | CR847960           | BX936345           | AC115592           | AC156865           | AB101022           | AB101021           | AC116957_1         | AC116957_0         | CR394545           | PFMAL13_25         | AX347043          | CR855390           | AX345795          | AC162359           |
| AX767564 Sequence |          | AX344713 Sequence | CQ807186 Sequence | CQ806912 Sequence | L36891 Saccharomyc | AY701231 Orconecte | CR847902 Danio rer | AC128556 Rattus no | BX294132 Zebrafish | AC117176 Dictyoste | AB101024 Carabus m | CR388102 Danio rer | CR847960 Danio rer | BX936345 Danio rer | AC115592 Dictyoste | AC156865 Bos tauru | AB101022 Carabus m | AB101021 Carabus m | Continuation (2 of | AC116957 Dictyoste | CR394545 Zebrafish | Continuation (26 c | AX347043 Sequence | CR855390 Danio rer | AX345795 Sequence | AC162359 Bos tauru |

## ALIGNMENTS

| TITLE JOURNAL REFERENCE AUTHORS   | #1797 E  | AUTHORS TITLE JOURNAL REFERENCE AUTHORS  | SOURCE<br>SOURCE<br>ORGANISM  | RESULT 1 AC129567 LOCUS DEFINITION ACCESSION VERSION   |
|---|--|--|---|--|
| Direct Submission Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 228046) Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., | Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cack, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand, Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamatt, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Mylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Pirer, S., Simmer, A. and Zody, M. | Birren,B., Nusbaum,C. and Lander,E. Mus musculus chromosome 8, clone RP23-50L10 Unpublished 2 (bases 1 to 228046) Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., | Mus musculus (house mouse) Mus musculus Mus musculus Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Muridae; Mus. 1 (bases 1 to 220046) | AC129567 228046 bp DNA linear ROD 06-APR-2004<br>Mus musculus chromosome 8, clone RP23-50L10, complete sequence.<br>AC129567<br>AC129567.8 GI:46240921 |

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                                    CTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTGTGTTCCCAGAAGGCTTCTGCAGTACA 166248
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on complement(15813..16133)
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17613..172
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Pred. No. 1.8e-270;
0; Mismatches 1;
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CE 1 (bases 1 to 228774)

CE 1 (bases 1 to 228774)

RS Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Desper, H., Dugan-Rocha, S., Dumn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Hanelarson, N., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kovar, C., Kovar, C., Liu, J., Liu, Y., Loudseged, H., Lovado, R., Johnson, R., Jolivet, A., Kangath, S., Lu, K., Manlloy, K., Mangum, A., Mahinderne, M., Mahinder
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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Rattus norvegicus clone CH230-187J8,
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AL Submitted (13-MAX-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:22857247.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-ecaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Rat Genome Sequencing Consortium.
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Direct Submission
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.) NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
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                                                                                                                                                                                                                                                                                                                                                   Center project name: GKWK
Center clone name: CH230-18708
Center clone name: CH230-18708
Center clone name: CH230-18708
Assembly program: Atlas 3.0;
Consensus quality: 215732 bases at least Q40
Consensus quality: 217275 bases at least Q30
Consensus quality: 218412 bases at least Q30
Consensus quality: 218412 bases at least Q30
Consensus quality: 218412 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Best Local Sin
Matches 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGTCTTCCCAGTACCGATCTCTGCAGCATTAACTTCTAGTCATGAAGGGGTGGTGACTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
TGGCTGGTCTGTGTTCCCAGAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCAC
                                                                                              GCCCCAGCTACTCTCTAGGAAATAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTG
                                                                                                                                           GCCCCAGCTTCTCTCTAGGAAATAATTAGGGTGCTGTGCCTATGACATGCCCAGGGGTCTTG
                                                                                                                                                                                                                            CCTAAAAAACAAACAAACAAACAAAAAAAAACCAGAAACTTTCCCTATGCTTTAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                ACCAAATACCAACAAGACTTTACTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTT 526
                                                                                                                                                                                   AGCCTTTATATTTACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATT
                                                                                                                                                                                                                                                                                                                                                                                          ---AAAAACCAGCAGAACTTTACTTCCCTTTGGAAAAACACAATTTTAAGGGCCGATCTT 83329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTAATAATATCAAACTGGGTTAAAAT---AAAAAAAATGTGCATAACTTAAAAAAAAA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATTCTGTGTTAAAGGTAAAAACATGTAAGTGCTGAG--AAGCTGACCTGATAACTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACTCAACAGACAATTAATCAGGCCAAACTACTTTAAGTTTTATTTGTGTATTTAAATGG 83155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTGAAGGAAAAGGTGTATGTTTGTTTCCTCTCGACATACTTCACTCAAAATATCTATTGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGCCAGGGGCTTTTTGAACTTAAATTAAAAGGGGAAAGTGATTTGCCTGAGCCCACTGAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GGACCAGAGCCACAGAGCTGGAAGTGTCTTTAGAAGTCAGTGTAGCCCCCAGCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTOTGCACAGTACCAATCTCTGGAGCATTAACTTCTAGTCATGAAGGGGTGGTGACT--
                                                                                                                                                                                                                                                                                                         ACTCTTTATATTTACAATAAAGAAAATAAACCA--GTCCTAATATAGCTGTAGTTTTATT 8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-----TTAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTGGTAACTTGA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGAAGGAAAAGGTATA----TGTTTCCTCTTGATATACCTCATTCAAATATCTATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by the finished sequence as soon as it is available the accession number will be preserved.

1 228774: contig of 228774 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="wgs_contig"
227275. .228774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="CH230-187J8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.0%;
85.0%;
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                                                                                                                                                                                                                                                          ------AAAAGAACAGAAACTTTCACTATGCTTTAAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 793.4; DB 14; Pred. No. 2.1e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 228774;
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AC132960
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VERSION
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bersato, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, C., Chen, C., Chen, Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84036 AAGAATGTG 84044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC132960
AC132960.3 GI:25073326
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus clone CH230-162J3, ***, 16 unordered pieces. AC132960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCAGGACTCCTATGTGCCTGCAAGTTTGCTGAACTCACAGTTTAGAACCCAAAGAGAGA 84035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGCAGACCTCTGGAGTGAGCAGGGCTGCTCCTTTCCTCTCAGGACAGCTCCGAGTGTGC
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В 8 밁 S 밁 á 밁 8 밁 Ś 밁 Ś

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Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., McLeod, M.P., McNeill, T.Z., Meenen, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mangum, B., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, P., Pondexter, A., Popovic, D., Primus, E., Pul, -L., Ploper, P., Condexter, A., Popovic, D., Primus, E., Pul, -L., Ploper, P., Conderer, A., Redilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walter, B., Walker, B., Wang, J., Warren, J., Warren, R., Weix, White, F., Wang, O., Wang, S., Warren, J., Warren, R., Weix, M., Walte, F., Walter, R., Wolley, K., Williams, G., Willson, R., Wieczyk, R., Mooden, H., Worley, K., Williams, G., Willson, R., Wieczyk, R., Mooden, H., Worley, K., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Nicelerhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Nicelerhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23322544.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-caffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome spatial contigs will be indicated in the feature
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Baylor Plaza, Houston, TX 77030,
3 (bases 1 to 32699)
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Rat Genome Sequencing Consortium.
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COMMENT

Center project name: KCDZ

Center clone name: CH330-162J3

Center clone name: CH330-162J3

Assembly program: Phrap; version 0.990329

Consensus quality: 276174 bases at least Q30

Consensus quality: 28235 bases at least Q30 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation Center code: BCM Center: Baylor College enter: Baylor College of Medicine

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces

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FEATURES
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322400: gap of unknown length
323510: contig of 1341 bp in length
323510: gap of unknown length
323510: contig of 1110 bp in length
323610: gap of unknown length
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227430

120

227313

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Indels

79;

Gaps

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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Castle, A., Colangelo, M., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Doglavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Porrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, C.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Tehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirreil, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
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Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome
                                            Zimmer, A. and Zody, M. Direct Submission
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1 (bases 1 to 191377)

Birren,B., Linton,L., Nu

Homo sapiens chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACO18398 191377 bp DNA linear PRI 30-APR-
Homo sapiens chromosome 8, clone RP11-16G12, complete sequence
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me 8, clone
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RP11-16G12
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Research, 320 Charles Street, Cambridge, MA 02141, USA
CE 4 (bases 1 to 191377)
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslawkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Wacdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldzim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nyoyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Roman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ve, W. J., Young, G.,
Direct Submission
AL. Submitted (30, APR-2002) Whitehead Institute/MTT Center for Genome
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3 (bases 1 to 191377)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pietre,N.,
Hagos,B., Horton,L., Hulne,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlanga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Viel,R., Vo,A., Wilson,B., M.X., Wyman,D., Ye,W.J., Young,G.,
Direct Submission
Al., Submitted (19, ADR-2002) Whitchead Institute/MTT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 19, 2002 this sequence version replaced gi:20148178. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                            Center project name: 13535
Center clone name: 16_G_12
                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="8"
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24043
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23908
                                                                                                                                                                                                                     /rpt_family="MIR"
complement(22452.
/rpt_family="MIR"
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/note="<30 qual SNGL region"

complement (6732. .6840)

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complement (9592.
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9061. .9174
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complement(1277. .142
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/clone_lib="RPCI-11 Human
/. .221
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17230
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732. 1803
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      family="LTR67"
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                                                                                                                                                                                                                                                                                                                                         41008 TTTCCCTCTGAAAAGGCACACGTTTACAGGAGCCAAACTTCTTCCTCTTTATTTGTAATA
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                                                                                                                                                                                TACAAACGAGCAGA--CAGACAACAGAGCCCCAGCT-ACTCTCTAGGAAATAATTA----
                                                                                                                                                                                                                                          GAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGCC 658
                                                                                                                                                                                                                                                                                                 AAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCTA-----AAAGAACA 598
                                                                                                                                                                                                                                                                                                                                                                                                                           ТАЛАЛА-----АЛАЛТСТССАТАЛСТТАЛАЛАЛАЛАССАЛАТАССЛАСЛАСАСТТТА 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG-AAACTGATGTTTCTAACGTGACTTAATAACAGATCTTTCTATCCAACTGTTCGGAAA
                                             CTGCAGCATGGGTCCTGGTTGGAGGGCAGGCATTCTGCTCTGATTTTTCCTGTTGCCTGG
                                                               CTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTTGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACACAGGCACTTAAATTCTAATTTCTCTATTGTAATGTAATGAACTTAATCAGTACA
                                                                                                                                   GGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCAGAAGGCTT
                                                                                                                                                                                                                      GGAACTTTCATTGTACTTCAACATTAAAGTTATTACCTCAGATATTTTGCCAGCTTAGCA
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28205. .28272
/rpt_family="GA-rich"
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/rpt_family="MLT1C"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Graham,L., Hagos,B., Heaford,A., Horton,L., Hulme,W., 11iev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Lamazares,R., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Stange-Thoman,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41488
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SEQUENCE, 22 u....
AC091095
AC091095.2 GI:14626897
AC091095.2 GI:14626897
AC091095.2 FULLTOP
                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 8, 2001 this sequence version replaced gi:13487963. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 183215)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson, Barran,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dwar,K., Collymore,A., Cooke,P., DeArellano,K., Dwar,K., Collymore,A., Cooke,P., DeArellano,K., Dwar,K., Dwar,K., Cooke,P., DeArellano,K., Dwar,K., Cooke,P., DeArellano,K., Dwar,K., Dwar
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1 (bases 1 to 183215)
5irren,B., Linton,L., Nusbaum,C.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                         Web site: http://www-seg.wi.mit.edu
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sapiens chromosome 8 clone RP11-77H21 map 8, WORKING DRAFT
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49957
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                                                                                                                         /clone="RP11-77H21"
/clone_lib="RPCI-11
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Consensus quality: 174312 bases at least consensus quality: 178687 bases at least Consensus quality: 180102 bases at least Insert size: 163000; agarose-fp Insert size: 181115; sum-of-contigs Quality coverage: 9.2 in Q20 bases; agaro Quality coverage: 8.3 in Q20 bases; sum-o
     sum-of-contigs
                            agarose-fp
                                                                                                 Q20
Q20
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\* NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contrys where the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

49245: contig of 49245 bp in length 49345: gap of 100 bp 49956: contig of 611 bp in length 'Qualifiers gap of 100 bp in length is contig of 10395 bp in length is gap of 100 bp contig gap of contig gap of gap of contig gap of contig gap of contig gap of gap of contig gap of contig gap of contig gap o conti gap of contig gap of contig gap of contig gap of contig gap of 100 bp contig of 1290 bp in length gap contig of 100 bp g of 1193 bp in length of 100 bp g of 1111 bp in length of 100 bp g of 725 bp in length f 100 bp g of 1617 bp in length f 100 bp g of 1440 bp in length 100 bp of 2423 bp in length 100 bp of 787 bp 100 bp of 915 bp 100 bp of 654 bp 100 bp of 994 bp in length 100 bp of 801 bp in length 100 bp of 653 bp in length 100 bp of 588 bp in length of 683 bp in length 100 bp of 719 bp in length of 27530 bp dq 001 in length in length in length in length

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| primer_bind    | /note="exon S" /note="exon S" | exon 34261. 34404 | exon 31357 GAON D | 1000  | <br>4 : insertion | mis complements | 0 · polymorphic back C     | 5 6 | primer_bind 10267log- primer_bind 10267l | polymo       | -392-222.probe"                    | .10240                        | 3                          | exon 1011510233 | =   | primer_bind 49914908<br>/note="5-391.rp complement" |            | er_bind     |           |             | /note≈"5-391-43.mis"<br>misc_binding 4589. 4613 | primer_bind 45824600               |                 | primer_bind 21082125 /note="5-390.rp complement" |   | .mis complement"   | tion 1999<br>/note="5-390-177 : polymo |                                    | inding       | /note="5-390.pu"<br>primer bind 19801998 | <pre>/note="5'regulatory region" primer_bind</pre> | misc_feature 12000                          | <pre>/organism="Homo sapiens" /mol_type="unassigned DNA"</pre> | FEATURES Location/Qualifiers source 1240825          | JOURNAL Patent: WO 0114550-A 1 01-MAR-2001; GENSET (FR) | Barry, C., Chumakov, I. and Blumenfeld, M. |
|----------------|-------------------------------|-------------------|-------------------|---|-------------------|-----------------|----------------------------|-----|--|--------------|------------------------------------|-------------------------------|----------------------------|-----------------|-----|---|------------|-------------|-----------|-------------|---|------------------------------------|-----------------|--|---|--|--|------------------------------------|--------------|--|--|---|--|--|---|--|
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| <u>.</u><br>4. | .67741<br>99-86.pu compl      | -                 |                   | 6/4636/48/<br>/bound_moiety="99-86-266.probe" | ٠.<br>و           |                 | /note="4-51.pu complement" | =   | =  | ۳٠.          | 4221342231<br>/note="4-51-312.mis" | 4212242141<br>/note="4-51.rp" | /note="4-54.pu complement" | =               |     | /bound_moiety="4-54-180.probe"                      | =          | 199 : po    | . 118"    | 1403        | 4137341397<br>/bound_moiety="4-54-199_probe"    | 4136641384<br>/note="4-54-199.mis" | /note="4-54.rp" | <u>.</u>   | = | <pre>/note="4-58-289 : polymorphic base G or C" 3997439992</pre> | /bound_moiety="4-58-289.probe" 39973   | /note="4-58-289.mls"<br>3996139985 | 39954. 39972 | Comp l                                   | .mis complement"                                   | 39944 // // // // // // // // // // // // / | 3993239956<br>/bound_moiety="4-58-318.probe"                   | 3925. 39943.<br>3925. 39943.<br>/notes"4-58-318.mis" | /note="exon T" 3987739896 /note="4.58 r)"               | 3970440858.                                |

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81241. .81265
                                                                                                                                                                                                                                                                                                                                                                                     /note="99-12738.pu"
81234. .81252
                                                                                                                                                                                                                                                                                                                                                                                                            /note="5-398.rp complement"
81006. .81025
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69509. .69533
/bound_moiety="4-88-107.probe"
69521
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76048. .76072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="exon
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75858. .75877
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72698. .72715
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                                                                    variation
                                                                                        misc_binding
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2001. .2079
/note="exon A"
2108. .2125
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Sequence 1 from Patent WO02066641.
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Pg-3 and biallelic markers thereof
Patent: WO 02066641-A 1 29-AUG-2002;
GENSET (FR)
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                                                                                                                              1980. .1998
/note="5-390-177.mis"
                                                                                                                                                                        1823. .1840
/note="5-390.pu"
                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="unassigned DN
/db_xref="taxon:9606"
note="5-390-177.mis
                                         note="5-390-177 : polymorphic base"
                                                                                     bound_moiety="5-390-177.probe"
                                                                                                                                                                                                                      note="5'regulatory region"
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| primer_bind  | primer_bind                  | variation               | misc_binding                                | primer_bind                                   | primer_bind | primer_bind           | variation               | misc_binding                                  | primer_bind                    | primer_bind                                  |                                    | primer_bind                  | exon                                      | exon   | exon       | exon   | primer_bind                               | variation | primer_bind                  | AUTTACTOIL                                  | mariation war                   | ה<br>ה      | primer bind                                    | primer_bind   | variation                | misc_binding                         | primer_bind  | exon                             | primer_bind                               | primer_bind              | exon .          | primer_bind | variation   | misc_binding | primer_bind  | primer_bind                               |
|--|------------------------------|-------------------------|---|---|-------------|-----------------------|-------------------------|---|--------------------------------|--|------------------------------------|------------------------------|---|--|------------|--|---|-----------|------------------------------|---|---------------------------------|-------------|--|---|--------------------------|--------------------------------------|--------------|----------------------------------|---|--------------------------|-----------------|-------------|-------------|--------------|--|---|
| /note="4-58.pu complement"<br>/note="4-58.pu complement" | 4-58-289 : pc<br>.39992      | "Clety="4-58-289.probe" | .39985                                      |   | ·           | 963<br>963<br>963 mig | moiety="4-58-318.probe" | .39956  | /notte="4-58.rp"<br>3992539943 | /note="exon T"<br>3987739896                 | /note="4-59.rp"<br>3970440858      | /note="exon S"<br>3955639574 | /note="exon F"<br>3737737466              | /note="exon E"<br>3426134404                   | 3135731471 | /10/08- 3-374.10 COMPLEMENT.<br>2681026897<br>/nofe="ayon D" | .10430                                    |           |                              | /note="5-392-280 : polymorphic base G or T" | /bound_moiety="5-392-280.probe" | "5-392      | /note="5-392-222.mis complement"<br>1026710285 | /Note="5-392-222 : polymorphic base G or I"<br>1022910247 | motery="5-392-222.probe" | /noce="5-392-222.m18"<br>10216.10240 | 10209. 10227 | /note="5-392.pu"<br>10115 10233  | /note="5-391.rp complement"<br>1000710025 | te                       | .mis compiement | , b         |             | 4589 .4613   | /HUCE="9-391.pu"<br>45824600<br>/note="5.191-43 mis" | /note="5-390.rp complement"<br>4599. 4577 |
| primer_bind  | exon                         | primer_bind             | variation                                   | misc_binding                                  | er_oin      | primer_bind           | primer_bind             | primer_bind                                   | variation                      | misc_binding                                 | primer_bind                        | primer_bind                  | primer_bind                               | primer_bind                                    | AGETACTON  | misc_pinding   | ול היים היים היים היים היים היים היים היי |           | primer bind                  | exon  | primer_bind                     | primer_bind | variation                                      | misc_binding  | primer_bind              | primer_bind                          | primer_bind  | primer_bind                      | variation                                 | misc_binding             | er_bin          | variation   | primer_bind | misc_vinding | rind:  | primer_bind                               |
| 7309973117<br>/note="5-397.rp complement"<br>7585875877  | 7288172918<br>/note="exon H" | =                       | /note="5-397-141 : polymorphic base G or T" | /2826/2850<br>/bound_moiety="5-397-141.probe" | =           | .72715<br>"5-397.pı   | omp1                    | 6952269540<br>/note="4-88-107.mis complement" | "4-88-107 :                    | 6950969533<br>/bound moiety="4-88-107.probe" | 6950269520<br>/note="4-88-107.mis" |                              | 6772467741<br>/note="99-86.pu complement" | 6747667494<br>/note="99-86-266.mis complement" | =          | 6/4636/48/<br>/bound_moiety="99-86-266.probe"                | 0/4300/4/4<br>/note="99-86-266.mis"       | 3         | /note="exon G"<br>6728967309 | /note="4-51.pu complement"<br>5043650545    |                                 |             | "4-51-312 : po                                 | 4222042244<br>/bound_moiety="4-51-312.probe"              | ¨=                       | =                                    | =            | .41423 "4-54-180.mis complement" | : polym                                   | 41416<br>d_moiety="4-54- | "-              | =           | 13 -        | 1            |  | 4113741154<br>/note="4-54.rp"             |

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                                                                                                                                                  CTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCCTAC
                                                                                                                                                                                                      AATGCCCAGGGTCCTGTAACAGATCGGTTTTTCCCCAGAGGGTTTCTGCAGCATGGGTCC 157975
                                                                                                                                                                                                                                  CATGCCCAGGGGTCTTGTGGCCTGGTCTG-TGTTCCCCAGAAGGCTTCTGCAGTACACAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAAAAAAAAAAAAAAAAAAAAAAAAAGTTTGTATTCCTCTTTCTACACAGACACTT
TATCAACTTATCATATAAGGGAAGGAAAGTGATTGATTCGGATACTGACACTGTAGACTC
                                      AGGAAGATAACGGCTAAGCCAGGAGGGGGGGAGCAGCCCACTACACATGTCTGGCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                       CTTCAACATTAAAGTTATTACCTCAGATATTTTGCCAGCTTAGCACGGCAAAAAATCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTCCTGACCTATTTGTAGTATTTTTATTCCTAAAGGAAAAAACAGGAACTTTCATTGTA 158155
                                                                    AGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="5-398.pu"
75989. .76151
/note="exon I"
76041. .76059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="99-12738-248.mis"
81241. .81265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="5-398.rp complement"
81006..81025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="5-398-203.mis complement"
76289. .76306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="5-398-203 : polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bound_moiety="5-398-203.probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="5-398-203.mis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           moiety="99-12738-248.probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .76072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 238; DB 6;
Pred. No. 2.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 265; Indels
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                                                                                     Query Match
Best Local
                                                                      Matches
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                              244 AAGGAAAAGGTGTATGTTTGTTTCCTCTCGACATACTTCACTCAAATATCTATTGTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6714 bp DNA linear
Homo sapiens angiopoietin-2 (AGPT2) gene, promoter
and partial cds.
AY563557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 6714)
Fiedlar, U., Hegen, A., Augustin, H.G. and Koidl, S.
Direct Submission
Submitted (04-MAR-2004) Vascular Biology and Angiogenesis Research,
Tumor Biology Center Freiburg, Breisacher Str. 117, Freiburg 79106,
                                                                                        l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression of Angiopoietin-2 in Endothelial Cells is Controlled by Positive and Negative Regulatory Promoter Elements (er) Arterioscler. Thromb. Vasc. Biol. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 6714)
Hegen,A., Koidl,S., Weindel,K., Marme,D., Augustin,H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol type="genomic DNA
/db_xref="taxon:9606"
/chromosome="8"
/map="8p23.1"
                                                                                                                                                         /note="Tie2-ligand"
/codon_start=1
/codon_start=1
/product="angiopoietin-2"
/protein_id="AAT69979.1"
/protein_id="AAT69979.1"
/db_xreff="GI:50082538"
/translation="MWQIVFFTLSCDLVLAAAYNNFRKSMDSIGKKQYQVQHGSCSYT
/translation="MWQIVFFTLSCDLVLAAAYNNFRKSMDSIGKKQYQVQHGSCSYT
                                                                                                                                                                                                                                                                                      4905. .>5192
/gene="AGPT2"
                                                                                                                                                                                                                                                                                                                                             /product="angiopoietin-2"
4428. .4904
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                                                                                                                                                                                                                                                                                                                          'gene="AGPT2"
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                                                                                       19.5%;
                                                                      Score 237.4; DB 8
Pred. No. 4.8e-44;
0; Mismatches 251
                                                                                                        DB 8;
                                                                                                    Length
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                                                                       Gaps
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                                                                                                                                                                                                                                                                   BC027216
Mus musculus ang
IMAGE:3494566),
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi, Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 2471)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Schuler,G. Klausner,R.D., Collins,F.S., Wagner,L., Schaefer,C.F., Bhat,N.K. Rlausner,R.D., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K. Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsich,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
                                                                                                                                                                                   MGC.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                    BC027216
BC027216.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAAGTGATTGATTCGGATACTGACACTGTAGGATCTGGGGGAGAGAGGACAAAGGACC
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1. 12473021
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Series: IRAK Plate: 30 Row: b Collumn: 12
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Filbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by: Baylor College of Medicine Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="MGC:25292 IMAGE:3494566"
/tissue_type="Mammary tumor metastatized to lung. The arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
FLLPETDSCRSSSSYMSNAVQRDAPLDYDDSVQRLQVLENILENNTQWLMKLENYIQ
DNMKKEMVEIQQNVVQNQTAVMIEIGTSLLNQTAAQTRKLTDVEAQVLNQTTRLELQL
LQHSISTNKLEKQILDQTSEINKLQNKNSFLEQKVLDMEGKHSEQLQSMKEQKDELQV
                                                                                                                                                                                                                                                                                                                                                                              /note="Bynonyms: Ang2, Ang-2"
/db_xref="geneID:11601"
/db_xref="MGI:1202890"
238..1728
                                                                                            /Godon_start=1
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/product="Appt: protein"
/protein id="AAH27216.1"
/db_xref="GI:20070844"
/db_xref="GeneID:11601"
/db_xref="GeneID:11601"
/db_xref="GeneID:11601"
/db_xref="GeneID:11601"
/db_xref="MWGI:1202890"
/translation="MWGIIFLTFGWDLVLASAYSNFRKSVDSTGRRQYQVQNGPCSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Lu29"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="Agpt2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="Czech II"
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Mus musculus angiopoietin-2 mRNA,
AF004326
                                                                                                                                                                                          Direct Submission
Submitted (16-MAY-1997) Discovery,
Old Saw Mill River Rd., Tarrytown,
                                                                                                                                                                                                                                              2 (bases 1.to 2424)
Maisompierre, P.C., Suri,C., Jones, P.P., Bartunkova,S.,
Wiegand,S.,J., Radziejewski,C., Compton,D., Aldrich,T.H.,
Papdopoulos,N., Daly,T.J., Davis,S., Sato,T.N. and Yancopoulos,G.D.
                                                                                                                                                                                                                                                                                                                                             angiogenesis
Science 277 (5322), 55-60 (1997)
                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 2424)
Maisompierre, P.C., Suri, C., Jones, P.F., Bartunkova, S.,
Wiegand, S.J., Radziejewski, C., Compton, D., Aldrich, T.H.,
Papdopoulos, N., Daly, T.J., Davis, S., Sato, T.N. and Yancopoulos, G.D.
Papdopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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                       /mol_type="mĸwa
/db_xref="taxon:10090"
/tissue type="uterine"
/clone_Tib="mouse uterine cDNA library (Clontech)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Agpt2"
/note="filament; Region:
/db_xref="CDD:pfam00038"
1072. .1719
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EQTTFRDCAEIFKSKLITTSGIYTLTFPNSTEEIKAYTUNDLKGGGGWTVU QHREDGSVD
FQRTWKEYKEGFGSPLGEYWLGNEFVSQLTGGHRYULKIQKDWEGNBAHSLVDHFYL
AGEESNYRIHLTGLTGTAGKISSISQPGSDFSTKDSDNDKCICKCSQMLSGGWWFDAC
/note="Ligand for the Tie2/Tek receptor tyrosine kinase; Method: conceptual translation with partial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Agpt2"
/note="FBG; Region: Fibrinogen-related domains (FReDs)"
/db_xref="CDD:smart00186"
                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                      Location/Qualifiers
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Pred. No. 7e-44;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
CCE 1 (bases 1 to 221218)

Pecora; Bovidae; Bovinae; Bos.

RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, C., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Baldwin, D., Barber, M., Barnstead, M., Benahmed, F., Blown, C., Baldwin, D., Blair, J., Blair, J., Blair, G., Burch, P., Brown, M., Benahmed, F., Biswallo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Center, A., Cardenas, V., Carter, K., Calderon, E., Cardenas, V., Carvez, D., Chan, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chan, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Duspar, H., Duspar, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Glil, R., Gardy, M., Guerra, W., Hartis, B., Haladin, W., Hamilton, K., Hanilton, K., Harles, S., Hladun, S.L., Hodgson, A., Hogues, M., Harlson, R., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kully, S., Khan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C.,
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Bos taurus
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAGAGCTCAGGACGCAAGTTTGCTGAACT 180
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/protein_id="AAB63189.1"
/db_xref="GI:2257931"
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clone CH240-8B21,
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Pred. No. 2.2e-38;
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, 27 unordered
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Nwaokelemeh, O., Okwoonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Pepovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Reeves, K., Regier, M.A., Reigh, R., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Revter, M., Rose, R., Ruiz, S.J., Reilly, B., Reilly, M., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Sateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Walter, R., Wang, J., Wang, G., Wang, S., Warren, R., Wei, M., Walter, B., Wang, J., Wang, J., Walter, B., Wang, J., Wang, J., Zhou, J., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                        and whole genome shotgun sequencing reads assembled using Atlas (http://www.lgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindarrne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Pal, S., Parks, K.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Pal, S., Parks, K.,
* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This is a 'working draft' sequence. It currently
                                                                             Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 26, 2005 this sequence version replaced gi:58037895. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 221218)
Cow Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                              Center: Baylor Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record
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RESULT 12
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            H. Bapiens CpG island DNA ge forward read cpg164g8.ftla. Z57119 .1 GI:1028350
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Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus. 1 (bases 1 to 132392) Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C.,
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                                                                                               AC141003
AC141003.1 GI:28875862
HTG; HTGS_PHASE1.
Rattus norvegicus (Norway rat)
                                                                                                                                                              AC141003 132392 bp DN
****, 64 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
Vector: pGEM-5Zf(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P. Purification of CpG islands using a methylated Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CpG island; genomic Mse1 fragment Homo sapiens (human)
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Dodsworth, S.J., Huc
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 7.5e-30;
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Morris, S., Moleod, M., Menen, E., Moya, M., Ouiroz, J., Rachlin, E.,
Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A.,
Popoyic, D., Pinus, E., Put, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Center: Baylor College of Medicine
Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GXKS
Center clone name: CH230-526115
Center clone rame: Pragic Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
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length

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\* NOTE: Estimated insert size may differ from sequence length

\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.)

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 64 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will Consensus quality: 98530 bases at least Q40 Consensus quality: 105678 bases at least Q20 Consensus quality: 110755 bases at least Q20 Estimated insert 8ize: 86014; sum-of-contigs estimation Quality coverage: 1x in Q20 bases; sum-of-contigs estimation

\_data.html).

as soon as it be preserved. 30449 30549 31895 31995 33379 33379 34876 34976 20895 22417 22517 23540 23740 23740 24843 24943 26029 26029 27719 9070 9170 10302 10402 11938 12038 12038 13407 13507 14991 14991 15091 16108 16208 16208 17286 17286 17384 18964 36003 27819 29222 29322 7850 7950 5659 6672 6772 1019 1119 2165 31894: 31994: 36002: 36102: 37499: 34875: 34975: 30448: 18963 16107 24842: 20894 19063 6771: 7849: gap of contig contig gap of contig unknown of 1590 unknown of 1403 unknown of 1078 unknown unknown of 1346 unknown of 1127 of 1123 unknown of 1017 unknown of 1484 unknown of 1078 of 1013 unknown of 1076 unknown of 1086 unknown of 1103 unknown of 1522 of 1731 unknown of 1578 of 1369 of 1536 unknown of 1132 of 1120 unknown of 1013 unknown of 1005 of 1046 of 1018 bp in length unknown length unknown unknown / bp in length
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                        wezquita,J., Mezquita,P., Montserrat,P., Vilagrasa,X. and Mezquita,C. Genomic structure and alternative splicin angiopoietin-2
           Biochem.
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Sequence 187 from Patent
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                                                                                                                                                             other sequences; artificial sequences
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                                                                    1. .2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Codon_start=1
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/protein_id="CAC08180.1"
/db_xref="GI:10120298"
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                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="angiopoietin-2"
476. .>763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
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1. .763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="angiopoietin-2"
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76.7%;
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Pred. No. 2.6e-22;
0; Mismatches 56
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WO0246454
        genomic
                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                                                                                                                              linear
       (Homo sapiens)"
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| Sear<br>Job   | 음 성   | 음 성   | 음 성   | 음 성   | 유 성  | 용 경  | 용 성   | 용왕  | M B   |
|---|---|---|---|---|--|--|---|---|---|
| ch c  |   |   |   |   |  |  |   |   | Best Lo<br>Matches  |
| omple<br>: 63   | 926<br>1950   | 867<br>1890   | 807<br>1830   | 748<br>1770   | 695<br>1710  | 635  | 582<br>1590   | 522<br>1530   | S C   |
| Search completed: December 12, 2005, 14:03:08<br>Job time : 6377 secs | 26 AAGGAAAGTGATTGGATACTGACACTGTAGACTCAGGGGAGAAACAAAGA<br> | 67 GG-GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCTTATCAACCTATCATATAAGGG<br> | 07 GCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGGAAGATAGTGGGTGAGCCA<br> | 48 TGGTCTG-TGTTCCCAGAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTAT | 95 TCTCTAGGAAATAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGC | 35 CTCAGATACTCTGCAAGCTTAGCCTACAAACGAGCAGAGACAGAC | 82 TTATTCCTAAAGAACAGAAACTTTCACTATGCTTTAAAATTAAAGTGATTAC<br> | 22 ATCITAGCCITTATATITACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATT<br> | l Similarity 62.1%; Pred. No. 1.1e-21;<br>295; Conservative 0; Mismatches 164; Indels 16; |
|   | AGA 980<br>   <br>ATA 2004                                | TATAAGGG<br>       <br> ATAAGGA                                     | STGAGCCA<br>      <br>  TAAGTTA                                     | AGCACTAT  | CTTGTGGC<br>    <br> TTGTAAT                             | CCAGCTAC   | STGATTAC<br>  | CTGTAATT  | ; Gaps  |
|   |   | 925<br>1949   | 866<br>1889   | 806<br>1829   | 747<br>1769  | 694<br>1709                                      | 634<br>1649   | 581<br>1589   | 4;  |

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                 December 12, 2005, 10:36:32 ; Search time 757 Seconds (without alignments)
10740.984 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|---------------|-------|----------------|-----------------------|----|----------|--------------------|
| 1             | 1220  | 100.0          | 1220                  | 12 | AD043367 | Ado43367 Mouse Ang |
| N             | 276   | 22.6           | 2475                  | 14 | ADZ61847 | Adz61847 Murine Ag |
| c<br>3        | 238   | 19.5           | 240823                | 10 | ADD69391 | Add69391 Human PG- |
| C 4           | 238   | 19.5           | 240825                | 4  | AAF24497 | Aaf24497 Human PG- |
| ი<br>5        | 238   | 19.5           | 240825                | δ  | ABQ81802 | Abg81802 Human PG- |
| 6             | 213   | 17.5           | 2424                  | 12 | ADQ09378 | Adq09378 Murine An |
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| 9             | 211.8 | 17.4           | 62705                 | 12 | ADQ09371 | Adq09371 Human Ang |
| 10            | 156.6 | 12.8           | 3251                  | œ  | ABX63024 | Abx63024 Human cDN |
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| 12            | 140.6 | 11.5           | 2846                  | σ  | ABQ67157 | Abg67157 Human ang |
| c 13          | 139.4 | 11.4           | 2846                  | 0  | ABQ67158 | Abg67158 Human ang |
| c 14          | 58    | 4.8            | 2000                  | 8  | ADA71938 | Ada71938 Rice gene |
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|               | 54.4  | 4.5            | 15698                 | σ  | ABL34141 | Abl34141 Human imm |
|               | 52.6  | 4.3            | 2265                  | 14 | ADW10467 | Adw10467 Colon pro |
| C 18          | 51.6  | 4.2            | 6523                  | σ  | ABN80121 | Abn80121 Human che |
| c 19          | 51.6  | 4.2            | 6523                  | 10 | ADE84216 | Ade84216 Human lym |
|               |       |                |                       |    |          |                    |

Disclosure; SEQ ID NO 1; 69pp; English.

angiogenesis.

WPI; 2004-365502/34.

New polynucleotide comprising a first nucleic acid encoding a light-generating gene product and a second nucleic acid encoding a selectable marker, useful in identifying a compound capable of modulating

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| 45                 | 44                 | 43                 | 42                 | 41                 | 40                 | 39                 | 38                 | 37                 | 36                 | 35                 | 34                 | (J)                | 32                 | 31                 | 30                 | 29                 | 28                 | 27                 | 26                 | 25                 | 24                 | 23                 | 22                 | 21                 | 20                 |
| 48.4               | 48.4               | 48.4               | 48.6               | 49                 | 49                 | 49                 | 49                 | 49                 | 49                 | 49                 | 49.2               | 49.8               | 50                 | 50                 | 50                 | 50                 | 50.2               | 50.8               | 50.8               | 51.2               | 51.2               | 51.6               | 51.6               | 51.6               | 51.6               |
| 4.0                | 4.0                | 4.0                |                    | 4.0                |                    | 4.0                | 4.0                | 4.0                | 4.0                |                    | 4.0                | 4.1                | 4.1                | 4.1                | 4.1                | 4.1                | 4.1                | 4.2                |                    |                    | 4.2                | 4.2                | 4.2                | 4.2                | 4.2                |
| 4661               | 4661               | 4661               | 487                | 8900               | 8900               | 8758               | 6127               | 6127               | 6127               | 2000               | 13784              | 15479              | 4415               | 4415               | 4415               | 4415               | 9964               | 6101               | 6101               | 20486              | 20486              | 6823               | 6523               | 6523               | 6523               |
| σ                  | σ                  | σ                  | ø                  | 13                 | 13                 | δ                  | 7                  | 6                  | 6                  | 11                 | σ                  | 6                  | 7                  | 6                  | 6                  | 6                  | 0                  | 13                 | 13                 | 7                  | 6                  | δ                  | 13                 | 13                 | 10                 |
| AAS61136           | ABL70185           | ABK31226           | ACH18710           | ADS89411           | ADS89685           | ABL33118           | ADS99710           | ABL70120           | ABL34449           | ACL37108           | ABK40062           | ABK39964           | ADS99863           | ABL70423           | ABL34602           | ABL33906           | ABL32099           | ADS89416           | ADS89690           | ADS99872           | ABL34611           | ABL33144           | ADS89346           | ADS89620           | ADE84140           |
| Aas61136 Human gen | Abl70185 Chemicall | Abk31226 Signal tr | Ach18710 Human adu | Ads89411 Oligonucl | Ads89685 Oligonucl | Abl33118 Human imm | Ads99710 Complemen | Abl70120 Chemicall | Abl34449 Human met | Acl37108 Rice stre | Abk40062 Human che | Abk39964 Human che | Ads99863 Bisulphit | Ab170423 Chemicall | Abl34602 Human met | Abl33906 Human imm | Abl32099 Human imm | Ads89416 Oligonucl | Ads89690 Oligonucl | Ads99872 Complemen | Abl34611 Human met | Abl33144 Human imm | Ads89346 Oligonucl | Ads89620 Oligonucl | Ade84140 Human lym |

## ALIGNMENTS

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RESULT 1
AD043367
ID AD04
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24-JUL-2003; 2003US-00627075.
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                                                                                                                                                                                                                                                                                                                                                                                              Livingston DM,
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/note= "Includes translation initiation codon at 3' end"
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CC The present sequence is that of the cis-acting regulatory region of the curvine Ang-2 gene located 5' to the start of transcription. This cis-acting DNA regulates preferential expression in endothelial muscle cells of a polypeptide-encoding DNA to which it is operably linked. The cis-envention provides compositions that include a polynucleotide encoding a reporter gene (e.g. a light-generating moiety), a polynucleotide encoding a selectable marker (e.g. an antibiotic) and optionally a regulatory claim of it that retains the ability to effect transcription of sequences, or a portion of the sequences in endothelial cells. The composition is used for imaging cultumour growth, engraftment and/or metastasis can be monitored by cobserving light emitted from the light-generating gene product. Also conserving light emitted from the light-generating gene product. Also cells, cells from established cell lines, or tumour cells) comprising the vector or polynucleotides, and transgenic animals and methods for their clanentification of a compound capable of modulating angiogenesis or which case transduction mathway.
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CAPACGAGCAGACAGACAGAGCCCCAGCTACTCTCTAGGAAATAATTAGGGTGGTGC
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Best Local Similarity
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                                                               fusion protein; fibrinogen-like; coiled-like domain; angiopoletin-related factor; ARF; angiopoletin; Ang-1; Ang-2; Ang-3; Ang-4; Ang-2X; vulnerary; antiinflammatory; vasotropic; necrosis; ischaemia; inflammation; wound healing; CCD; FLD; human; PG-3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a methods for screening biologically active agents, such as candidate drugs, to determine whether the agent possesses a defined biological activity. The methods involve making one or more comparisons chosen from comparing efficacy value of agent to reference efficacy value, comparing a toxicity value of the agent to reference toxicity value, comparing a classifier value of the agent to
                                                                                                                                                                                       Human PG-3 DNA
                                                                                                                                                                                                                                                                                                                           ADD69391 standard; DNA; 240823 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2475 BP; 724 A; 589 C; 642 G; 520 T; 0 U; 0 Other;
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Pred. No. 2.4e-62
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein comprising a fibrinogen-like or coiled-like domain, useful for preparing a composition for treating necrosis, ischemia or inflammation, or for promoting wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel fusion protein comprising a fiblike domain (FLD) or coiled-coil domain (CCD). The domain may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 127; 340pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTCTAATTTCTCTATTGTAATGTAATGAACTTAATCAGTACAGTGTATTTTTAGAGT
CATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCCAGAAGGCTTCTGCAGTACACAGTC
                                    TCAGACAAAAGAGATCAACTGCTCTCTAGGAAATACTTAATTGGGGTGGTGCCTAGGA
                                                                    ACAGACAACAGAGCCCCA-GCTACTCTAGGAAA----TAATTAGGGTGGTGCCTCTGA
                                                                                                                                  CTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGCCTACAAACGAGCAG--
                                                                                                                                                                                                                                                        GCACACGTTTACAGGAGCCAAACTTCTTCCTCTTTATTTGTAATAACAAAAATAAACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATATCCAAGTGGAGTTTTTTTAAAGA-ATAAAGGTCAGAGCTCAG-AAACTGATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCACTCAAATATCTATTGTTACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTT
                                                                                                         CTTCAACATTAAAGTTATTACCTCAGATATTTTGCCAGCTTAGCACGGCAAAAATCAGTT
                                                                                                                                                                                 AGTCCTGACCTATTTGTAGTATTTTTATTCCTAAAGGAAAAAACAGGAACTTTCATTGTA
                                                                                                                                                                                                                                                                                         GCACATTTACAAGGG----CTGATCTTAGCCTTTATATTTACAATAAAGAAAATAAACCAA
                                                                                                                                                                                                                                                                                                                                 ACTTGGCTAGTGGTTCAAGAATCAACTAAAATCAATGAATCTATTTTTCCCTCTGAAAAG 158273
                                                                                                                                                                                                                                                                                                                                                           AATGTGCATAACTTAAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCCTTGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                      CTAACGTGACTTAATAACAGATCTTTCTATCCAACTGTTCGGAAATGAAAATCTTTTGTA 158333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAAAAAAAAAAAAAAAAAAAAAAAAAAGTTTGTATTCCTCTTTCTACACAGACACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 238; DB 10;
Pred. No. 2.1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265;
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| primer_bind           | allele                               | misc_binding                       | primer_bind | primer_bind             | primer_bind          |                       | exon   | C            | CDS<br>Primer Prima |             |                                  | misc_binding | primer_bind            | primer_bind                            | FH Key FT misc_feature FT  | Kev                         | man; FG-3; C                       | man FG-3 gen | -MAY-2001               | F24497; | . acaidatu;             | 4<br>17/C<br>F24497  | 157732 AAGTGAGC | 1025 AGGACAGC    | 792  | 965   | 157852 TATCA  | 905 TATC         | AGGA   | 157972 TGGT1  | 786  | 158032 AATG  |
|-----------------------|--------------------------------------|------------------------------------|-------------|-------------------------|----------------------|-----------------------|--|--------------|---------------------|-------------|----------------------------------|--------------|------------------------|--|----------------------------|-----------------------------|------------------------------------|--------------|-------------------------|---------|-------------------------|--|-----------------|------------------|--|---|---|------------------|--|---|--|--|
| complement (46024620) | /noce= "binds probe" replace(4601,G) | 7 CAGE K<br>45894613               | <u>.</u>    | 4559. 4577<br>/*tag. 45 | 2108 125<br>/*tag= : |                       | /product= "PG-3"<br>/note= "this sequence contains introns"<br>2001 2070 | ,            | " 6                 |             | /*tag= d<br>/note= "binds probe" | 19872011     | /*tag= b<br>1980. 1998 | /note= "5' regulatory region" 18231840 | 12000<br>12000<br>/*tag= a |                             | ancer; BRCAl; chromosome 8p23; ds. |              | (first entry)           |         | aid; CDNA; 240825 BP.   |  | AGC 157725      | 7AGC 1032        | TGGGGAGAGAAGGAACAAAGGACCGTĠAAAGCTĠCTCTĠTAAÁAĠCTGACACAGCCCTCCC 157733 | AGGGGAGAAAACAAAGAGTCCGTGCAGACCTCTGGAGTGAGCAGGGGCTGCTCCTTCCT | TATCAACTTATCATATAAGGAAAGGAAAGTGATTGATTCGGATACTGACACTGTAGGATC 157793 | 964              | GGAAGATAACGGCTAAGCCAGGAGGGCGGAGCACTACACTTCGCTGCTCTTCTCTCTC | TGGTTGGAGGGCAGGCATTCTGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTAC 157913 | CTTTGGGGCAGTAAGCACTATGCTCTGATTTTTTCCTGTTGCCTGGCTAGTGACCCCCCTAC 845 | AATGCCCAGGGGTCCTGTAACAGATCGGTTTTTCCCAGAGGTTTCTGCAGCATGGGTCC 157973 |
| E FI                  | 1 1 1 1<br>2 2 2 2                   | H H I                              | F F         | F F                     | 1 1<br>2 2           | FT T                  | FTT  | F) F)        | F F '               | F 17 .      | 1 T T                            | FI           | n n                    | 1 H H                                  | E F                        | # H T                       | 5 F F                              | 7 H F        | 1111                    | 1 79 79 | ı Fi                    | 리 리 리 리<br>리 리 리 리   | 1 T T           | E I              | 1 1 1  | FIT   | FT  | F T              | FT FT  | 된 11 H  | 11.1   | FT   |
| primer bind           | allele<br>primer bind                | 't                                 | J           |                         |                      | primer bind           | allele   | misc_binding | primer_bind         | primer_bind | exon                             | ٠,'          | primer bind            | exon                                   | ехоп                       | exc.r                       |                                    | exon         | primer_bind             | allele  | primer_bind             | allele   |                 | primer bind      | primer_bind  | allele  | misc_binding  | primer_bind      | exon   | primer_bind   | primer_bind  | S  |
| /*tag= ar             | replace( /*tag= compleme             | /*tag= "                           |             |                         | /*tag=               | /*tag= al             | /note= "   |              |                     |             | 39704<br>/*tag=                  |              | /label=                | /label=<br>37377.                      | 34261.<br>/*tag=           | /*tag=<br>/*tag=<br>/lahel= | /label=                            | 26810.       | /*tag=<br>10411.        | /*tag=  | complem                 | /*tag=<br>/note=<br>replace<br>/*tag=                              |                 | /*tag=<br>10267. | /*tag=<br>complem  | /note=<br>replace   | 10216.<br>/*tag=  | 10209.<br>/*tag= | 10115.<br>/*tag=   | /*tag=<br>10007.  | /label=<br>4891.   | /*tag=   |
| ar<br>ar              | بر<br>ا                              | /*tag= ap<br>/mote= " hinds probe= | ao          | an<br>39972             |                      | al<br>al 39945 30963) | note= " binds probe"<br>/note= " binds probe"                            | .39956       | .39943              |             |                                  | ah           | 3057/                  |  |                            | .31471<br>ad<br>8           |                                    | .26897       | /*tag= aa<br>1041110430 |         | complement (1028710305) | <pre>/*tag= x /note= "binds probe" replace(10286,T) /*tag= v</pre> | w<br>.10298     |                  | /*tag= u<br>complement(1022910247)                                   | <pre>/note= " binds probe" replace(10228,T)</pre>           |   |                  | .10233   |   | - B<br>.4908   |  |

38;

Gaps

11;

340

158513 280

158453

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replace(42232,C)
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replace(72838,T)
/*tag= bz
                                                                                                                            /"cag= bs
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replace(41404,C)
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/note= "binds probe"

replace(67475,G)
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67289. .67309

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67456. .67474

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41564
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69609. .69626
/*tag= bv
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69502.
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/*tag= bh
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41385.
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                                                                                                                                                                                                                                                                                                                                                                                           504 GCACATTTACAAGGG----CTGATCTTAGCCTTTATATTTTACAATAAAGAAAATAAACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 GTAACTTGATTTAATAA-------AA
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                                                                                                                                                                                                                                                            TCAGACAAAAGAGATCAACTGCTCTCTAGGAAATACTTAATTGGGGTGGTGCCTAGGA
                                                                                                                                                                                                                                                                                                   AAGTGAGC 157727
                                                                                                                                                                               TGGTTGGAGGGCAGTCTGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                 GCACACGTTTACAGGAGCCAAACTTCTTCCTCTTTATTTGTAATAACAAAAATAAACCGA
                                          AGGACAGC 1032
                                                             TGGGGAGAGAGGAACAAAGGACCGTGAAAGCTGCTCTGTAAAAAGCTGACACAGCCCTCCC
                                                                               AGGAAGATAACGGCTAAGCCAGGAGGGGGGGGGGGCAGCCCACTACACATGTCTGGCTGCTCT
                                                                                                                                                    AGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCT
                                                                                                                                                                                           CTTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTTGCCTTGGCTAAGTGACCCCCCTAC
                                                                                                                                                                                                                                     CATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCAGAAGGCTTCTGCAGTACACAGTC
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                                                                                                                                                                                                                                                                                                                CTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGCCTACAAACGAGCAG---
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72881. .72918
/*tag= cb
/label= H
73099. .73117
/*tag= cc
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503 158335 443 158395 400

158275

671 158155 613

1024

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157855

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157975

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ID ABQ81802;
AC ABQ81802
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                                                                  primer_bind
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/*tag= dj

4582. .4600

/*tag= dk

4*tag= dk

4589. .4613

/*tag= ni

/note= "probe"

4601
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complement(2108.
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10209.
/*tag=
10216.
/*tag=
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4627. .4718
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/note= "probe"
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/number= 2
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/standard_n
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/*tag= dm
10007. .10025
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719. .10114
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/note= "polymorphic base G or C; the nucleotide is give
/note= "polymorphic code in the specification"
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Best Local Similarity
Matches 213; Conserv
                                                                          Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic; antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a compound targeted to a nucleic acid molecule encoding the human Angiopoletin-2 polypeptide. The compound is an arisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioatte linkage, at least one modified sugar moiety, preferably a 2.0-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human Angiopoletin-2 polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents DNA encoding the murine Angiopoletin-2 polypeptide of the invention.
   CDS
                                           BUM
                                                                                                                        Mouse angiopoietin-2 (Ang-2) encoding
                                                                                                                                                           02-DEC-2004
                                                                                                                                                                                                             ADS13802 standard; DNA; 2424 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide compound that inhibits expression of Angiopoietin-2, useful for preparing a composition for treating hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 13;
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GENBANK; AF004326.
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P-PSDB; ADQ09609.
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                                                                  therapy; mouse; gene; Ang-2; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                        (first entry)
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Location/Qualifiers 211. .1701
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Pred. No. 1.2e-45;
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                                                                                                                                                                                                                                                                                                                                        CC pharmaceutical carrier and an amount of an extracellular matrix (ECM).
CC binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also
CC provided are methods of treating an individual suspected of having
CC coronary artery disease, vascular disease or a condition involving
CC ischaemia; of promoting angiogenesis, endothelial survival and
CC individual suspected of having a disease related to lack of blood vessels
CC related to lack of blood vessels such as ischaemia in hearts and limbs;
CC artherosclerosis risk by maintaining the patients with the diseases
CC vessels; to assist the recovery of the patients who had stroke and the
CC cells and establish endothelial monolayer and inhibit excessive
CC vessels to assist the restenosis by inhibiting re-closure of blood
CC vessel after inserting stents into blood vessels; to make stable and
CC vessel after inserting stents into blood vessels; to make stable and
CC vessel after inserting stents into blood vessels; to make stable and
CC vessel after inserting stents into blood vessels; to make stable and
CC vessel after inserting stents into blood vessels; to make stable and
CC vessel after inserting stents into blood vessels; to make stable and
CC dabetes and/or arthritis in an individual suspected of being at risk of
CC disease, vascular disease and disorders, e.g. cancer, coronary artery
CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
CC angiogenesis, or arthritis. The present sequence represents the mouse Ang
CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
CC -2 encoding DNA.
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                                                                                                                                                                                                                                                                  Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 34; 114pp; English
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CACAGTTTAGAACCCAAAAAGAGAGAGAGAATG
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                                  ACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAGAGCTCAGGACGCAAGTTTGCTGAACT
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                                                                                                                                                                                                                                                              ilarity 100.0%; I Conservative 0;
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/product= "Ang-2"
                                                                                                                                                                                                                                                                                                                                      709 A; 581
                                                                                                                                                                                                                                                                          17.5%; Score 213; DB 13; 100.0%; Pred. No. 1.2e-45;
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 181
CACAGTTTAGAACCCAAAAAGAGAGAGAGAGAATG 213
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ADU39008 standard; cDNA; 2424 ВP

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ADU39008;

27-JAN-2005 (first entry)

Mouse Ang2 cDNA

type I diabetes, antiangiogenic, cytostatic, antidiabetic, ophthalmological, nephrotropic, neuroprotective, cardiant, vasotrogene therapy, cholesterol, endometrial neovascularisation, tumour, diabetic retinopathy, age-related macular degeneration, gene, ss. small interfering RNA; siRNA; Ang1; g1; Ang2; Tic cytostatic; Tie2; angiogenesis; inhibitor; vasotropic;

Mus musculus.

WO2004094606-A2

04-NOV-2004

19-APR-2004; 2004WO-US012072

18-APR-2003; 2003US-0463981P

(UYPE-) UNIV PENNSYLVANIA.

Reich SJ,

Tolentino

2004-795558/78

New isolated small interfering RNA (siRNA) comprising a sense RNA strand and an antisense RNA strand, useful for treating angiogenic disease, e.g diabetic retinopathy or age-related macular degeneration.

Claim 2; SEQ ID NO 5; 182pp; English

CC comprises a sense RNA strands form an RNA duplex, where the sense RNA strand and an antisense RNA strand. The sense and CC comprises a nucleotide sequence substantially identical to a target Sequence of 19-25 contiguous nucleotides in human Angl. Ang2 or Tie2 CC further comprises: a recombinant plasmid comprising nucleic acid Sequences for expressing an siRNA comprising a sense RNA strand and an CC antisense RNA strand; a recombinant viral vector comprising nucleic acid sequences for expressing an siRNA comprising a sense RNA strand and an CC antisense RNA strand; a pharmaceutical composition comprising siRNA, the plasmid, or the viral vector and a pharmaceutical carrier; a method of cinhibiting expression of human Angl. Ang2 or Tie2 mRNA, or an alternative splice form, mutant, or cognate; a method of inhibiting angiogenesis in a composition comprising a subject; and a complex strand and an anglogenesis in a subject; and a subject; and a complex strand and an complex stran The invention relates to a novel isolated small interfering from type I diabetes in a subject comprises RNA (siRNA)

The invention relates to a compound targeted. The onucleic acid molecule encoding the human Angiopoietin-2 polypeptide. The compound is an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage

nucleic

Claim 1; SEQ ID NO 4; 102pp;

English

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ09371 standard;
                                                                                                                                                                                                                            disorder,
                                                                                                                                                                                                                                                New oligonucleotide compound that inhibits expression of Angiopoietin-2, useful for preparing a composition for treating hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                             Myers K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Angiopoietin-2; gene; ds; antisense oligonucleotide; phosphorothioate linkage; 2'.O-methoxyethyl sugar moiety;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Angiopoietin-2 DNA #4
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RESULT 10
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Best Local
28-JUL-2000;
08-JAN-2001;
                                                                                                                                                  hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
                                      08-JAN-2002;
                                                                                            US2002137081-A1
                                                                                                                                                                                                   Human; gene;
                                                                                                                                                                                                                          Human cDNA #24 differentially expressed
                                                                                                                                                                                                                                                         25-FEB-2003
                                                                                                                                                                                                                                                                                                           ABX63024 standard; cDNA; 3251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'.O-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human Angiopotetin.2 polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents DNA encoding a human Angiopotetin-2 polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                         1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 AAAGAACAGAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
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                                                                                                                                                                                                                                                                                                                                                                           GTAAAAGCTGACACAGCCCTCCCAAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                   GAGCAGGGCTGCTCCTCTCAGGACAGC 1032
                                                                                                                                                                                                                                                                                                                                                                                                                            TCGGATACTGACACTGTAGGATCTGGGGAGAGAGGAACAAAGGACCGTGAAAGCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGATACTGACACTGTAGACTCAGGGGAGAAACAAAGAGTCCGTGCAGACCTCTGGAGT 100:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGCTTCTGCAGTACACAGTCCTTTGGGGCCAGTAAGCACTATGCTCTGATTTTTTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TAATTAGGGTGGCTCTGACATGCCCAGGGGTCTTGTGGGCTGGTCTG-TGTTCCCA 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTAGCCTACAAACGAGCAG--ACAGACAACAGAGCCCCA-GCTACTCTCTAGGAAA--
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2000US-0222469P
2001US-0260483P
                                       2002US-00044090
                                                                                                                                                                                          ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                            ВP
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Pred. No. 1e-44;
                                                                                                                                                                                                                        in activated vascular
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                                                                                                                                                                                                                       tissue
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CC discloses a high throughput method for detecting differentially expressed CC cDNAs in a sample. The cDNAs of the invention may have cC cDNAs in a sample. The cDNAs of the invention may have cC synaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-cC cDNAs in a sample, or screening several molecules or compounds to the cC cDNAs in a sample, or screening several molecules or compounds to the protein. A protein encoded by the cDNA may be used to screen several molecules or compounds to the protein, or to produce or purify an antibody to the protein, or to produce or purify an antibody to the protein from a sample. The nucleotides may be useful for cC diagnosing, staging, treating, or monitoring the progression of treatment cC disease, hypertension, diabetes, pre-cclampsia, ischaemia-reperfusion cC diagnosing pre-pathologic disorders, pre-cclampsia, ischaemia-reperfusion cC diagnosing pre-pathologic disorders, and chronic or acute diseases genetic or gene expression analysis of several new nucleic acid compounds to the protein. The present sequence represents a cDNA of the invention of the protein. The present sequence represents a cDNA of the invention confidence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a combination comprising several differentially expressed in activated vascular tissue. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comporises several cDNAs that are differentially expressed in activate vascular tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BAND/) BANDMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Page; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNAs that are invention also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activated
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Query Match Sequence 3251 BP; 1083 A; 645 C; 674 G; 849 T; 0 U; 0 Other;

Best Local

Similarity

74.9%; 12.8%;

Length 3251;

S 밁 δ 밁 Ś 밁 δ 밁 Ś Matches 252 192 934 132 874 815 72 12 209; TCTGGAGTGAGCAGGCTGCTCCTTCCTCAGGACAGC 1032 GAGCAGCCCACTACACATGTCTGGCTGCTCTTATCAACTTATCATATAAGGAAAGGAAAG GCTGCTCTGTAAAAGCTGACACAGCCCTCCCAAGTGAGC TGATTGATTCGGATACTGACACTGTAGGATCTGGGGGAGAGAGGAACAAAGGACCGTGAAA TGATTGATTCGGATACTGACACTGTAGACTCAGGGGAGAAACAAAGAGTCCGTGCAGACC TTTTCCTGTTGCCTGGCTAGTGACCCCCCTACAGGAAGATAACGGCTAAGCCAGGAGGGCG TTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGGAAGATAGTGGGTGAGCCAGG-GGGCG TGTTCCCAGAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTATGCTCTGAT Conservative , , Score 156.6; DB 8; Pred. No. 1.2e-30; Mismatches 69; 290 Indels 1: Gaps 933 131 873 71 191 814

RESULT 1 ADD69421 ID ADD

ADD69421 standard; DNA; 763

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RESULT 12
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Best Local S
Matches 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel fusion protein comprising a fibrinogen-
like domain (FLD) or coiled-coil domain (CCD). The domain may be
identical or homologous to that of an angiopoietin-related factor (ARF),
examples of which include Ang (angiopoietin)-1, Ang-2, Ang-4, Ang-4 and
Ang-2X. The molecules of the invention demonstrate vulnerary,
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 763 BP; 202 A; 183 C; 205 G; 173 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angiopoietin-related factor; ARF; angiopoietin; Ang-1; Ang-2; Ang-3;
Ang-4; Ang-2X; vulnerary; antiinflammatory; vasotropic; necrosis;
ischaemia; inflammation; wound healing; CCD; FLD; human; ds; Ang-2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory and vasotropic activities whilst the fusion protein may be useful for preparing a composition for treating necrosis, ischaemia or inflammation, as well as for promoting wound healing. The current sequence is that of the human Ang-2A DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 157; 340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003048185-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for preparing a composition for treati
inflammation, or for promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kessler PD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENV-) GENVEC INC.
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                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                 1028 ACAGC 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; fibrinogen-like; coiled-like domain;
                                                                                                                                                                                                                                                     AAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGCCTGCACATGTCTGGCTGCTCTTAT
                                                      TGAGC
                                                                                                                GGAGAGAGAACAAAGGACCGTGAAAAGCTGCTCTGTAAAAGCTGACACAGCCCCTCCCAAG
                                                                                                                                         CAACTTATCATATAAGGAAAGGAAAGTGATTGATTCGGATACTGACACTGTAGGATCTGG
                                                                                                                                                                                                  CAACTTATCATATAAGGGAAGGAAAGTGATTGATTCGGATACTGACACTGTAGACTCAGG
                                                                                                                                                                                                                                AAGATAACGGCTAAGCCAGGAGGGGGGGGGAGCCCACTACACATGTCTGGCTGCTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein comprising a fibrinogen-like or coiled-like domain, preparing a composition for treating necrosis, ischemia or
                                                                                                                                                                                                                                                                                                                                                  Conservative
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76.7%;
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Pred. No. 2e
                                                                                                                                                                                                                                                                                                                                                               .4; DB 10;
2e-27;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
diagnosis or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2846 BP;
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748 TGGTCTG-TGTTCCCAGAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTAT
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                                                                                                                                                                                                                                                                                                    295;
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                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                           TTATTCCT-----AAAAGAACAGAAACTTTCACTATGCTTTAAAATTAAAATGAGTGATTAC
                                                                                                          TTTAGATATTTTGTTAGTTTAGTACGGTAAAAATTAGTTTTAGATAAAAGAGATTAATTG
                                                                                                                                          TTTTTTTAGGAÀATÀTTTÀATTGGGGTGGTGTTTAGGAAATGTTTAGGGGGTTTTGTAAT
                                                                           TCTCT----AGGAAATAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGC
                                                                                                                                                                         ATCTTAGCCTTTATATTTACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATT
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                                                                                                                                                                                                                                                                                                                                                                871 A; 45 C; 651 G; 1279 T; 0 U; 0 Other;
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RESULT 13
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KW Inflam
KW Antiar
XX Homo 8
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                                                                                                                                                                                                           The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I) also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
diagnosis or treatment of cancer.
                                                                                                                                                                                 Sequence 2846 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 188; 41pp + Sequence Listing; German.
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                                                                                                                                                                        759 A; 45 C; 565 G; 1477 T; 0 U;
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                                                           Score 139.4; DB 6;
Pred. No. 4.2e-26;
0; Mismatches 316;
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TAACACTATAAAATCTAAAAAAAAAAAAAACA
                          TGACACTGTAGACTCAGGGGAGAAACAAAGA 980
                                                     CTAGTGACCCCTACAGGAAGATAGTGGGTGAGCC-AGGGGGCGGAGCGGCTGGCTGCAC
                                                                                                                                                                         CTACAACATAATCCTAATTAAAAAACAACATTCTACTCTAATTTTTCCTATTACCTAA
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2000 BP; 336 A; 265 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27;
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Quan .
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                                                                                                                           MWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKG
                                                                                                                                                                                KRAKRSYRYRRRWYWKRKGWTYRYRYWRSCRMTRARMSKRRKWAGASMKSCWMYWRGARS
                                                                                                                                                                                                        GATTACCTCAGATACTCTGCAAGCTTAGCCTACAAAC--GAGCAGACAGACAACAGAGCC
                                                                                                                                                                                                                                                                   TATAGCTGTAATTTTATTCCTAAAAGAACAGAAACTTTCACTATGCTTTAAAATTAAAGT
                                                                                                                                                                                                                                                                                                                                                                                    GCATAACTTAAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCCTTGGAAAAGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMSWTYAMWKKYTKYMTAYSSTWKWYWAYKWRAYAWSRSRKTWWCTGGKRMATYCGTKMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                      CCAGCTACTCTAGGAAATAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGG
                                                                                                                                                                                                                                         KKYATRYYWKMWAMTWWWSWRRWKSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARWT
                                                                                                                                                                                                                                                                                                MTKWWTTWACAWRATSWRWRAMAGMRWKRYKMKRAYWWRWWRCWKAGWARWMKSRYRWKW
                                                                                                                                                                                                                                                                                                                            TTTACAAGGGCTGATCTTAGCCTTTATATTTACAATAAAGAAAATAAACCAAGGTCCCGA
                                                                                                                                                                                                                                                                                                                                                        KWSWRRMYWTMTKWAWTWMTCMCMAKWYMATGWATWMWWRYTMYTYCYAMTCAKCKYKMA
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGRWRWRMAWCWYCCMWKWWKMTSCMWWKYWRTWSCWYTMWWGAMRYAYYAMRRRRWTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.8%;
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Pred.
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0.00013;
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Query Match
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Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10710 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer a disease, AIDS, province action of the matory, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory, Vulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL32893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPIGENOMICS
                                                                                                                       TAAAAAAAAATGTGCATAACTTAAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCC
                                                                                                                                                                                                              GTGAGTGCTGAGAAAACTGATGTTGGTAACTTGATTTAATAATATCAAACTGGGTTAAAA 435
                                                                                                                                                                                                                                                                                                                                                                                                   TATGTTTGTTTCCTCCGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATT
AAATACTTTCTAACATACAATTAACAAAAAAAATAAAAATTAATTCTCTCCATCCTC
                                                                                                                                                                           AATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTTAAGGCACAGACAT
                                                                                                                                                                                                                                                                                                                                                           TTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTACAATAAAGAAAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.5%;
48.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment of of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10710;
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| Search co<br>Job time         | 9        | γQ      |
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| completed: D<br>ne : 762 secs | 5316 AAC | 556 ACC |
| December 12,<br>cs            | 5314     | 558     |
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1220
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9b est4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                               gb_est1:*
gb_est2:*
gb_est3:*
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Pred. No., is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 22        | 21       | 20         | 19       | 18        | 17       | 16        | 15        | 14       | 13        | 12                 | 11         | 10       | 9        | 80        | 7        | 6         | ហ         | .4       | ω         | 2         | <b>-</b> | Result      |
|-----------|----------|------------|----------|-----------|----------|-----------|-----------|----------|-----------|--------------------|------------|----------|----------|-----------|----------|-----------|-----------|----------|-----------|-----------|----------|-------------|
| 93.8      | 119.6    | 121.8      | 133.2    | 133.6     | 143.4    | 149       | 167.8     | 175.8    | 178.6     | 185.8              | 203.4      | 204      | 208.6    | 217.8     | 240.4    | 242       | 253       | 263      | 274.4     | 276       | 276      | Score       |
| 7.7       | 9.8      | 10.0       | 10.9     | 11.0      | 11.8     | 12.2      | 13.8      | 14.4     | 14.6      | 15.2               | 16.7       | 16.7     | 17.1     | 17.9      | 19.7     | 19.8      | 20.7      | 21.6     | 22.5      | 22.6      | 22.6     | Query       |
| 247       | 679      | 466        | 592      | 477       | 482      | 921       | 525       | 204      | 726       | 793                | 661        | 665      | 276      | 912       | 299      | 2443      | 354       | 330      | 792       | 2475      | 699      | Length      |
| N         | N        | σ          | w        | N         | œ        | σ         | v         | N        | σ         | 11                 | 9          | N        | N        | N         | N        | 4.        | -         | N        | 7         | 4.        | UI       | BB          |
| BF085046  | BB614741 | CB548076   | BP320006 | BE292322  | DN994582 | CB203297  | BU580281  | BB601394 | BX506958  | CR905089           | AZ984331   | BB612537 | BB569161 | BE306402  | BB649745 | AK048622  | AA389106  | BB847613 | CN539462  | AK019860  | BY716819 | ID          |
| BF085046  | BB614741 | CB548076   | BP320006 | BE292322  | DN994582 | CB203297  | BU580281  | BB601394 | BX506958  | CR905089           | AZ984331   | BB612537 | BB569161 | BE306402  | BB649745 | AK048622  | AA389106  | BB847613 | CN539462  | AK019860  | BY716819 | Description |
| PM0-GN001 | BB614741 | AMGNNUC: C | BP320006 | 601084072 | TC119420 | AGENCOURT | ik77g09.y | BB601394 | DKFZp779M | CR905089 Sus scrof | .2M0265M18 | BB612537 | BB569161 | 601102294 | BB649745 | Mus muscu | mp24h01.r | BB847613 | UI-M-HUO- | Mus muscu | BY716819 | ion         |

| <b>4</b><br>5      | 44                | 43                 | c 42               | c 41               | 40                 | c 39               | c 38               | 37                 | c 36               | c 35               | 34                 | 33                   | c 32               | 31                 | c 30               | 29                 | c 28               | 27                | 26                 | 25                 | 24                 | 23                 |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| 52                 | 52                | 52.2               | 52.2               | 52.6               | 52.6               | 52.8               | 52.8               | 52.8               | 53                 | 53.2               | 53.6               | 54                   | 54.4               | 54.6               | 55                 | 55                 | 55.4               | 55.8              | 57.6               | 58.4               | 58.4               | 58.4               |
| <b>4.</b><br>ن     | 4.3               | 4.3                | 4.3                | 4.3                | 4.3                | 4.3                | 4.3                | 4.3                | 4.3                | 4.4                | 4.4                | 4.4                  | 4.5                | 4.5                | 4.5                | 4.5                | 4.5                | 4.6               | 4.7                | 4.8                | 4.8                | 4.8                |
| 1101               | 331               | 1201               | 1085               | 1201               | 759                | 1131               | 1043               | 978                | 639                | 1000               | 510                | 1101                 | 1150               | 1101               | 928                | 512                | 1101               | 454               | 532                | 834                | 819                | 804                |
| 10                 | _                 | 10                 | 10                 | 10                 | 11                 | Ľ                  | 10                 | 10                 | 11                 | 10                 | თ                  | 10                   | 10                 | 10                 | 10                 | v                  | 10                 | ۲                 | <u>-</u>           | 7                  | 7                  | 7                  |
| CNS0039V           | AU037151          | CNS0167M           | CNS02PW4           | CNS0167M           | CNS06QXV           | CNS034FO           | CNS0145P           | AG129148           | CNS038CX           | CNSOOCOQ           | BX478886           | CNS0021J             | AG365432           | CNS00EVL           | CNSOODKY           | BX504641           | CNS00EQL           | AV682744          | AI882255           | CO735207           | CO739225           | CO739081           |
| AL063936 Drosophil | AU037151 AU037151 | AL106396 Drosophil | AL208525 Tetraodon | AL106396 Drosophil | AL411257 T7 end of | AL227373 Tetraodon | AL103735 Drosophil | AG129148 Pan trogl | AL232458 Tetraodon | AL059446 Drosophil | BX478886 DKFZp686L | . AL061936 Drosophil | AG365432 Mus muscu | AL069706 Drosophil | AL071865 Drosophil | BX504641 DKFZp686M | AL069526 Drosophil | AV682744 AV682744 | AI882255 ul56c11.y | CO735207 SlLE04c10 | CO739225 S1LE04c22 | CO739081 SlLE04c22 |

ALIGNMENTS

RESULT 1 BY716819 LOCUS DEFINITION

| of 60,770 full-length CDNAs<br>of 80,770 full-length CDNAs<br>Nature 420, 563-573 (2002)   | JOURNAL            |
|--|--------------------|
| Arakawa, F., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shinagawa, A., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation | TITLE              |
| Tally, F., Edul, E., Edvoidi, F., & Liu, E., & Liu, E., & Cathilice, F., Hayatsu, N., Hirozane Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,   |                    |
| Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  |                    |
| Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K<br>Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita  |                    |
| Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran, Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwa  |                    |
| <pre>Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima, Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,</pre>  |                    |
| Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.  |                    |
| Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji H. Kawasawa Y. Kedzierski R. M. King R.L. Konagaya A.,  |                    |
| <pre>rieconer,C.r., rorrest,A., riazer,A.s., Gaasterrand,I., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,</pre>   |                    |
| Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A   |                    |
| Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsud<br>Batalov.S. Beisel K.W., Blake J.A., Bradt.D., Brusic.V.,  |                    |
| <pre>Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,</pre>  |                    |
| Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,   |                    |
| 1 (bases 1 to 699)   | REFERENCE          |
| Sciurognathi; Muroidea; Muridae; Murinae; Mus.   |                    |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                    |
| Mus musculus   | ORGANISM           |
| Mus musculus (house mouse)   | SOURCE             |
| B1/16819.1 G1:2/129936   | VEXULON<br>VEXULON |
|  | ACCESSION          |
| ovary and uterus Mus musculus cDNA clone 5031400E18 5', mRN  |                    |
| BY716819 RIKEN full-length enriched, 11 days pregnan   | DEFINITION         |
| BY716819 699 bp mRNA linear EST 17-DEC-2002  | LOCUS              |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                      Conservative
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                                                                                                                                                                                                                 /clone lib="RIKEN full-length enriched, 11 days pregnant adult female ovary and uterus"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="ovary and uterus"
/dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="5031400E18"
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on i of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2475)

Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., I Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., I
                                                                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sagaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramateu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                Functional annotation of a full-length mouse
                                                                                                                                                                                                                                                                        The RIKEN Genome Exploration Research Group Phase II Team
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                                                                                                                                                                                                                     Nature 409,
                                                                                                                                                                                                                                                           FANTOM Consortium.
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High-efficiency full-length cDNA cloning
Math. Enzymol. 303, 19-44 (1999)
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Please visit our web site (http://genome.gsc.riken.jp/) for further
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/proteIn_id="BAB31887.1"
/proteIn_id="BAB31887.1"
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EQTTFRDCAEIFKSGLTTSGIYTLTFPNSTEEIKAYCDMDVGGGGWTVIQHREDGSVD
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/dev_stage="11 days
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="11 days pregnant adult"
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AGEESNYRIHLTGLTGTAGKISSISQPGSDFSTKDSDNDKCICKCSQMLSGGWWFDAC
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(SWISSPROT|035608, evidence: FASTY, 99.6%ID, 100%length,
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/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
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Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 792)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is clone was contributed by the Brain Molecular Anatomy Project
/tissue_type="whole eye"
/dev stage="newborn( 1, 5, 15 days)"
/lab_host="DH10B (T1 phage resistant)"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP HU0"
/clone lib="NIH BMAP HU0"
/clone lib="NIH BMAP HU0"
/site 2: Not I; The library was constructed according
Site 2: Not I; The library was constructed according
Site 3: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with Oligo-dT
grimer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:30666956"
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REFERENCE
AUTHORS
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                          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira, and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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              and Hayashizaki
RIKEN integrat
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                                                                                                                                                                                                                                                               Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., 2001)
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sequence analysis (RISA) system--384-format
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Pred. No. 4.4e
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                                        Inoue, Y., Kira, A.
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 950 TGACACTGTAGACTCAGGGGAGAAACAAGAGTCCGTGCAGACCTCTGGAGTGAGCAGGG
Mus musculus
Mus musculus
Eukaryota; Me
                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266;
                                                 AA389106
AA389106.1 GI:2042062
EST.
                                                                                    mp24h01.rl Life Tech mouse embryo 8 5dpc 10664019 clone IMAGE:570193 5', mRNA sequence.
AA389106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    further details.
e mouse tissues.
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/dev_stage="adult"
/lab_host="SOLR"
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Pred. No. 2.8e-55;
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JOURNAL
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Best Local 9
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1 (bases 1 to 354)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                    AK048622
AK048622.1 GI:26339449
HTC; CAP trapper.
                                                                                                                     AK048622 2443 bp mRNA linear HTC 03-. Mus musculus 16 days embryo head cDNA, RIKEN full-length en library, clone:Cl30089A05 product:ANGIOPOIETIN-2 PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
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                                                                                                insert
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  musculus (house mouse)
                  CAP trapper
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                                                                                                sequence.
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/note="Organ: whole embryo; Vector: pcMV-SPORT2; Site
Sall, Site 2: Not1; Cloned unidirectionally. Primer:
Oligo dT. 8.5dpc embryos. pCMV-SPORT2 vector."
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/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:570193"
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Pred. No. 9.7e-53;
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                                                                           source
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E 6 (bases 1 to 2443)

Radachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiranoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, W., Hiranoto, K., Hiraoka, T., Horane, T., Hayashida, K., Hayatsu, W., Hiranoto, K., Kogawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagawa, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramateu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gs.gr.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                           URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboracory in R Division of Experimental Animal Research in Riken contribu
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FUNCtional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                   prepare mouse tissues.
Please visit our web site for further details
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                                            organism="Mus musculus'
/strain="C57BL/6J"
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Yokohama,
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BB649745
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SCHLOGUECULA, 199)

1 (bases 1 to 299)

Arakawa,T., Carrinci,D., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Hara,A., Kouda,M., Koya,S., Matauyama,T., Myazaki,A., Nomura,K.,
Konno,H., Kouda,M., Okido,T., Salto,R., Sakai,C., Sakai,K.,
Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
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                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
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Query Match Best Local S Matches 241

Similarity

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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-resegge.riken.jp, URL:http://genome.gsc.riken.jp/Carninci.p, Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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Conteact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RII Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKI 17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 2: Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Human Genome Sequences. Mamm. Genome. 10, 673-677 (2001)
            /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
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/sex="mixed"
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mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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1 (bases 1 to 912)
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Mus musculus
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National Institutes of Health, Mammalian Gene
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                  GTGAGCAGGGCTGCTCCTTCCTCAGGACAGCTCCGAGTGTGCCGGGGAGAAGAGAAGA 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop:
                                                                     Conservative
                                                                                                                                               /lab_nost="will CGAP_Lu29"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
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/site_2: NotI; Cloned unidirectionally. Primer: Oligo (
Site_2: NotI; Cloned unidirectionally. Primer: Oligo (
Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                 /tissue_type="spontaneous tumor,
Stem cell origin."
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/db_xref="taxon:10090"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                     clone="IMAGE:3494566"
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Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Alzawa, K., Akahira, S., Akimura, T., Hiraoka, T., Hirozane, T. Carninci, P., Hanagaki, T., Ishii, Y., Itoh, M., Izawa, M., Kawai, K., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Takahashi, F., Tanaka, T., Toya, T., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, Wuramateu, M., and Hayashizaki, Y., Tanaka, T., Toya, T., Tataka, Sato, Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
Tel: 81-45-503-9222
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
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BB569161 RIKEN full-length enriched, 17 days embr
musculus cDNA clone 3322402G22 5', mRNA sequence.
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                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3322402G22"
/tissue_type="head"
/dev_stage="17 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                     sex="mixed"
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Miyazaki,A.,
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Query Match
Best Local Similarity
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Ebarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

2E 1 (bases 1 to 665)
1 (bases 1 to 665)
RS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T.,
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
AL Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tanrumi-kn, Yokohama, Kanagawa, 230,0046
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Mus musculus (house mouse)
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Matches

JOURNAL COMMENT

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REFERENCE AUTHORS

SOURCE ORGANISM

KEYWORDS

ACCESSION VERSION

RESULT 10 BB612537

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DEFINITION

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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new prepare full-length cDNA libraries for rapid discovery of new wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

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CCCTGTGCCTTAGACAGCAGCTGAGAGCTCAGGACGCAAGTTTGCTGAACTCACAGTTTA 1196
                                                    GAAAGAGCCTGCTGCGGGACGGAGAAGGCTCTCACTGATGGACTTATTCACACGGCACAG
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                                                                                                                                                                 TTCCTCTCAGGACAGCTCCGAGTGTGCCGGGGAGAAGAGAAGAGAAGAGAGACAGGCACTGG 1076
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGAATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                           16.7%; or
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Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0265 row: M column: 18
Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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GSS.
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Contact: Robert B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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2M0265M18R Mouse 10kb plasmid UUGC2M library Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 661.
           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clome_lib="Mouse 10kb plasmid UUGC2M library"
/notce="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (Temale) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
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Best Local Similarity
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350 A-----GTATTTTGTGTTAAGGCACAGACATGTGAGTGCTGAGAAAACTGATGTTGGT 402
                                                      290 TATCTATTGTTACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTAT 349
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                                                                                                                                                                                                                                                                                                                                             Chardon, P., Iannuccelli, N., Roig, A., Dossat, C., Demars, J., Rogel-Gaillard, C., Roy, A., Schibler, L. and Milan, D. A. physical map of the swine genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Construction of a swine BAC library: application to the characterization and mapping of porcine type C endoviral elements Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
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Rogel-Gaillard,C., Bourgeaux,N., Billault,A.,
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (pig)
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                                TATGTATTATAATTTAGAGGGCCATTAATCAGTCCAGCATATTTTAAATTTACTTTGAAT 110
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                                                                                                 Conservative
                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="Large White"
/db_xref="taxon:9823"
                                                                                                                                                                             note="Genoscope sequence ID : IH0AAA34DD10FM1"
                                                                                                                                                                                                  /cell_type="fibroblast"
/clone_lib="SBAB"
                                                                                                                                                                                                                               'sex≃"male"
                                                                                                                                                                                                                                                clone="bI0352F04"
                                                                                                                                                                                                                                                                                                            organism="Sus scrofa"
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                                                                                              Score 185.8; DB 11;
Pred. No. 1.1e-35;
0; Mismatches 202;
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Pred. No. 3.9e-40;
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                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                                                                                                                                                                   BX506958 726 bp mRNA DKFZp779M112_r1 779 (synonym: hncc1) Hon DKFZp779M112_5', mRNA sequence.
                                                                               EST (Poustka,A., Albert,R., Moosmayer,P., Wellenreuther,R., et al.)
Unpublished (2003)
                                                                     Contact: MIPS
                                                                                                                                         Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wel
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G.,
                                                                                                                                                                                                                                                         Homo sapiens (human)
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1 (bases 1 to 204)
Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Hirozane, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Carninci, P., Hanagaki, T., Iahii, Y., Itoh, M., Izawa, M., Kawai, J., Hodoyama, Y., Imotani, K., Iahii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Okazaki, Y., Okada, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okado, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, A., Yasunishi, A., Yoshida, K., Yoshiki, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 bp mRNA linear
BB601394 RIKEN full-length enriched, 13 days embr
musculus cDNA clone D430011L06 5', mRNA sequence.
BB601394
                                                                                                                                                                                                                                                                     Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                     BB601394.1 GI:11509995
EST.
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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No s1 sequence available.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGATACTGACACTGTAGACTCAGGGGAGAAACAAAGAGTCCGTGCAGACCTCTGGAGTGA 1003
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/mol_type="mRNA"

/db xref="taxon:9606"

/clone="bKFZp779M112"

/tissue_type="liver"

/dev_stage="fetal"

/lab_host="pH108"

/clone_lib="779 (synonym: hncc1)"

/note="Vector: pSport1_Sfi; Site_1: Sf
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Pred. No. 7.4e-34;
0; Mismatches 79;
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.rtc.riken.go.jp) for
                                ACGCCACAGCCCTGTGCCTTAGA 1150
                                                                                                  AGGCACTGGGAAAGAGCCTGCTGCGGGACGGACGAAGGCTTTCACTGATGGACTTATTCAC 112
                                                                                                                                                          ACTGACACTGTAAAATCAGGGGAGAAACAAAGAGTCCGTGCAGAACTCTGGAGTGAGCAG
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                                                                             AGGGACTGGGAAAGAGCCTGCTGCGGGAGGGAGAGGGTCTCACTGATGGACTCATCCAC 181
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
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/dev_stage="13 days embryo"
/lab_host="DH10B"
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/clone="D430011L06"
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91.6%;
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                                                                                                                                                                                                                                                                                                                                             Score 175.8; DB 2
Pred. No. 2.9e-33;
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                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                       1102
                                                                                                              35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing b Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40RP from Gibco High quality sequence stop: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrine Pancreas Consortium Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MA 02138
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                            AGGCTCTCACTGATGGACTTATTCACACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAG 1161
                                                                                                                                           GCCGGGGAGAAGAGAAGAGAAGAGACAGGCACTGGGGAAAGAGACCCTGCTGCGGGACGGAGA 1101
                                                                                                              GCAGAGTACGGGGGAAGAGAGAGACAGGCACTGGGAAAGAGCCTGCTGCGGGACGGAGA 94
AGGCTCTCACTGATGGACTTATTCACACGGCACAGCCCTGTGCCTTAGACAGCAGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 525)
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Location/Qualifiers
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:10000"
/db xref="taxon:10000"
/dev stage="p.c. 14.5"
/lab_host="B. coli-pH12S (GIBCO)"
/clone_lib="Kaestner ngn3 wt"
/clone_lib="Kaestner ngn3 wt"
/clone_lib="Kaestner ngn3 wt"
/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
/note="Organ: pancreas; Vector: pSPORT1 (The pancreas was obtained from Gerard and been published. The pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000). The cDNA's were prepared with an oligo containing a NotI site, and SalI linkers were added to the ends. The inserts were cut with NotI before being cloned into the NotI-SalI sites in the vectors. This is one of two libraries, ngn3 wt and ngn3 -/-. The wt library is in pSPORTI, T7 promoter is 5'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="129/Sv x CD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                13.8%;
                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                Score 167.8; DB 5;
Pred. No. 3.7e-31;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                          Length 525;
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Scoring table:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     December 12, 2005, 12:00:02; Search time 260 Seconds (without alignments) 8340.866 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1303057 seqs, 888780828 residues
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1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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|-------------------|---------------------|---------------------|-------------------|-------------------|-------------------|-------------------|---------------------|--------------------|---------------------|---------------------|---------------------|-------------------|---------------------|---------------------|---------------------|-------------------|-------------------|--------------------|-------------------|-------------------|------|-------------------|-------------------|--------------|--------|
| 24                | 23                  | 22                  | 21                | 20                | 19                | 18                | 17                  | 16                 | 15                  | 14                  | 13                  | 12                | 11                  | 10                  | 9                   | œ                 | 7                 | σ                  | ហ                 | 4                 | w    | N                 | ۲                 | No.          | ult    |
| 40.4              | 40.6                | 40.6                | 41                | . 41              | 41.2              | 41.6              | 41.6                | 41.8               | 42                  | 42                  | 42                  | 42.2              | 42.4                | 42.4                | 42.6                | 43.8              | 44                | 44.6               | 45.4              | 45.4              | 46.2 | 46.4              | 47.4              | Score        |        |
| 3.3               | ω<br>               | ω.<br>ω             | 3.4               | 3.4               | 3.4               | 3.4               | 3.4                 | 3.4                | 3.4                 | 3.4                 |                     | 3.<br>5           | 3.5                 | 3.5                 | 3.5                 | 3.6               | 3.6               | 3.7                | 3.7               | 3.7               | 3.8  | 3.8               | 3.9               | Match        | Query  |
| 837               | 70323               | 601                 | 19124             | 244               | 0                 | 32392             | 280                 | 832                | 143550              | 601                 | 601                 | 50000             | . 95020             | 93493               | 80411               | 2308              | 1141              | 732                | 20674             | 20674             | 1141 | 1864              | 7218              | Match Length |        |
| w                 | w                   | w                   | N                 | ω                 | w                 | w                 | w                   | ω                  | w                   | w                   | w                   | w                 | w                   | ω                   | w                   | w                 | w                 | w                  | w                 | w                 | w    | w                 | Ν                 | . B          |        |
| US-08-998-416-288 | US-09-949-016-17594 | US-09-949-016-70227 | US-08-487-826B-13 | US-09-621-976-484 | US-09-662-254B-24 | US-09-662-254B-27 | US-09-621-976-14588 | US-09-621-976-2813 | US-09-949-016-14143 | US-09-949-016-83376 | US-09-949-016-83375 | US-09-662-254B-25 | US-09-949-016-13272 | US-09-949-016-12063 | US-09-949-016-15777 | US-10-104-047-682 | US-09-806-708B-22 | US-08-998-416-1036 | US-10-170-097-651 | US-09-641-638-651 | -09- | US-09-468-265-4   | US-08-232-463-14  | ID           |        |
|                   |                     | 702                 | 13,               | 4                 | 24,               |                   |                     |                    | Sequence 14143, A   |                     | 8337                | Sequence 25, Appl | 13272,              | 1206                | 157                 | 682,              | Sequence 22, Appl | Sequence 1036, Ap  | 651,              | e 651,            | 22,  | Sequence 4, Appli | Sequence 14, Appl | Description  |        |

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| 45      | 44                  | 43               | 42              | 41                  | 40                | 39               | 38                   | 37                  | 36                  | 35                  | 34                  | 33                  | 32                  | 31                  | 30                  | 29                  | 28                  | 27                | 26                  | 25                 |
| 39.8    | 40                  | 40               | 40              | 40                  | 40                | 40.2             | 40.2                 | 40.4                | 40.4                | 40.4                | 40.4                | 40.4                | 40.4                | 40.4                | 40.4                | 40.4                | 40.4                | 40.4              | 40.4                | 40.4               |
| ω<br>.υ | ω<br>ω              | 3.3              | 3.3             | ω<br>ω              | 3.3               | 3<br>3           | υ<br>. υ             | ω<br>ω              | ω<br>.ω             | 3.3                 | 3.3                 | ω<br>.ω             | 3.3                 | 3<br>3              | ω<br>.υ             |                     | ω<br>ω              | 3.3               | ω<br>.ω             | ω<br>. ω           |
| 19124   | 72278               | 7938             | 7286            | 921                 | 663               | 11748            | 601                  | 278866              | 278866              | 278866              | 278866              | 278866              | 278866              | 278866              | 278866              | 278866              | 278866              | 6996              | 1412                | 1412               |
| N       | w                   | w                | w               | ω                   | w                 | N                | ω                    | w                   | ω                   | w                   | w                   | w                   | w                   | w                   | ω                   | w                   | w                   | w                 | ω                   | w                  |
|         | US-09-949-016-16113 | US-09-331-581-14 | US-09-331-581-3 | US-09-248-796A-9583 | US-08-998-416-191 | US-08-611-107-30 | US-09-949-016-206713 | US-09-949-016-14703 | US-09-949-016-14702 | US-09-949-016-14701 | US-09-949-016-14700 | US-09-949-016-14699 | US-09-949-016-13926 | US-09-949-016-13925 | US-09-949-016-13924 | US-09-949-016-13923 | US-09-949-016-13922 | US-09-573-080A-29 | US-09-270-767-22773 | US-09-270-767-7491 |
|         | Sequence 16         | Sequence 14      | Sequence 3,     | Sequence 95         | Sequence 191      | Sequence 30,     | Seguence 20          | Sequence 14         | Seguence 14         | Sequence 14         | Sequence 14         | Sequence 14         | Sequence 13         | Sequence 13         | Sequence 13         | Sequence 13         | Seguence 13         | Sequence 29       | Sequence 22         | Sequence 74        |
| , Appl  | 16113, A            | , Appl           | Appli           | 9583, Ap            | 1, App            | , Appl           | 206713,              | 14703, A            | 14702, A            | 14701, A            | 14700, A            | 14699, A            | 13926, A            | 13925, A            | 13924, A            | 13923, A            | 13922, A            | 29, Appl          | 773, A              | 7491, Ap           |

## ALIGNMENTS

| FILING DATE: CLASSIFICATION PRIOR APPLICATION NUM APPLICATION NUM FILING DATE: APPLICATION NUM FILING DATE: APPLICATION NUM FILING DATE: APPLICATION NUM FILING DATE: APPLICATION FILIPATATION FILEFAX: FILECOMMUNICATION FILEFAX: FI | RESULT 1  US-08-232-463-14/c  ¡Sequence 14, Applicatio ¡Patent No. 5670367 ¡GENERAL INFORMATION: APPLICANT: SCHEIFLI APPLICANT: SCHEIFLI APPLICANT: FALKNER, TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE ADDRESSEE: Foley STREET: 1800 D149 COTTY: Alexandria COUNTRY: USA COUNTRY: USA COUNTRY: USA COMPUTER READABLE FO MEDIUM TYPE: Flop COMPUTER: DATE C |
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| FILING DATE:  CLASSIFICATION: 435 PRIOR APPLICATION UMBER: US/07/935,313 FILING DATE:  APPLICATION NUMBER: US/07/935,313 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:  NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELEPHONE: (703)836-9300 TELEFAX: (703)836-9300 TELEFAX: (703)836-9300 TELEFAX: (703)836-9300 TELEFAX: (103)838-109 TELEFAX: (103)888-109 TELEFAX: (103) | lication U 67 67 71ON: FORMER, F. CHEIFLINGE ALKNER, R. WITION: NTION: FE ADDRESS: FOLEY & L. 100 Diagona andria andria andria SA  |

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APPLICANT: Berka, Randy M
APPLICANT: Gullen, Daniel
APPLICANT: Gray, Gregory L
APPLICANT: Hayenga, Kirk J
APPLICANT: Hayenga, Kirk J
APPLICANT: Lawlis, Virgil B
ITITLE OF INVENTION: Heterologous Polypeptides Expressed in Filamentous Fungi, Proce
FILE REFERENCE: A-42909-5
CURRENT APPLICATION NUMBER: US/09/468,265
CURRENT APPLICATION NUMBER: US/09/468,265
CURRENT FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/284,942
PRIOR FILING DATE: 1994-08-02
PRIOR APPLICATION NUMBER: 07/413,010
PRIOR APPLICATION NUMBER: 07/413,010
PRIOR APPLICATION NUMBER: 07/163,219
PRIOR APPLICATION NUMBER: 07/163,219
PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 06/882,224
PRIOR FILING DATE: 1986-07-07
PRIOR APPLICATION NUMBER: 06/871,374
PRIOR APPLICATION NUMBER: 06/771,374
PRIOR APPLICATION NUMBER: 06/882,224
PRIOR FILING DATE: 1985-08-29
NUMBER OF SEQ ID NOOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
CRIGANISM: Emericalla nidulans
UNG-09-468-265-4
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   Query Match 3.8%; Score 46.4; DB 3; Best Local Similarity 45.4%; Pred. No. 0.005; Matches 167; Conservative 0; Mismatches 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09468265
Patent No. 6379928
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%; Score 47.4; DB 2; Length 7218;
llarity 0.8%; Pred. No. 0.0054;
Conservative 221; Mismatches 147; Indels 0
                               Length 1864;
   Indels
   0
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US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; Patent No. 6784342
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                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                   Local Similarity
nes 68; Conserv
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NAME/KEY: promoter; LOCATION: (1)..(1141); LOCATION: (1)..(1141); OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters US-09-806-708B-22
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TITLE OF INVENTION: Regulation of Embryonic Transcription in
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                           265 TTCCTCTCGACATACTTCACTCAAATATCTATTGTTACTTAACAGACAATTAATCAGGCC
                                                                                                                                                                                                                                                                                                                                                      793 BBCYRANNNNAARMARTCNNYMHAAVTTTHTDWCYKTWMNTWYWDMMTTMBTTTTRNMT
                                                                                                                                                                                                                                                                                                                                                                                                           205 GCCACAGAGTGATGAGCCCGAGGAAACCCCTGATACAGTGAAGGAAAAAGGTGTATGTTTGT
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VKWRDTTCTYVDVWADSWVWWYANWMRCRDVTYTRNNTYCKSYAHSYWYWSNNAMWYRRY 554
                                                        NTKTRWYSTTRRHHYTGÅTNNNNNNNNNNNNNNNSCCTCTRMMTMRWTMKGDGMTVRKK
                                                                                                                                                                                                                                   TSTNMTNNNNNMWACTNNNNNMWKAYYAHATNNWGCWWNNTDARRTNNTTVMRRRWMT
                                                                                                                                                                        AAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAAGGCACAGACATGTGAGTGCT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATAAATTCTAGAGTTTTATTAATTAGAGAAAGGGGATAATAATCTTTTTTAATAATAAT 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 46.2; DB 3;
11.2%; Pred. No. 0.0044;
ative 230; Mismatches 306;
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RESULT 4
US-09-641-638-651/c
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SEQ ID NO 651
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                                                                                                                                                                                                                                                                                                                                                                                                                      CUKKENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR ADDITOR TOWNERS
                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/133,200 PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
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                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER:
                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                 NAME/KEY: exon
LOCATION: 5552
                                                 OTHER INFORMATION: exon
                                                                 NAME/KEY: exon
LOCATION: 3871..4072
                                                                                                   LOCATION: 3124..3297
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chumakov, Ilya
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NAME/KEY: allele LOCATION: 2934 OTHER INFORMATION: 1 NAME/KEY: allele LOCATION: 2947
                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1559
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 1570
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OTHER INFORMATION: 10-508-245 :
NAME/KEY: allele
                                                                                                                               LOCATION: 2832
OTHER INFORMATION:
                                                                                                                                                            LOCATION: 2623
OTHER INFORMATION:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173
NAME/KEY: allele
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OTHER INFORMATION: exon
                                                                                     LOCATION: 2844
OTHER INFORMATION:
                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 2341
                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 2323
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OTHER INFORMATION: exon 11
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                                                                                                                   NAME/KEY: allele
                                                                                                                                                                                                      NAME/KEY: allele
                                                                                                                                                                                                                      OTHER INFORMATION: 10-512-36
                                                                                                                                                                                                                                                                OTHER INFORMATION: 10-511-337
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
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LOCATION: 17555..20674
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 INFORMATION: 10-513-365
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LOCATION: 121/.
OTHER INFORMATION: 7
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LOCATION: 6019
OTHER INFORMATION: 10-346-141
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263
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LOCATION: 4088
OTHER INFORMATION: 12-206-366
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278
                                                       LOCATION: 8926
OTHER INFORMATION:
                                                                               NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION: 10-347-165
NAME/KEY: allele
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OTHER INFORMATION: 10-347-74 :
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111
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NAME/KEY: allele
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LOCATION: 8608
OTHER INFORMATION: 10-349-47
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OTHER INFORMATION: 10-349-97 :
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LOCATION: 8658
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LOCATION: 6611
OTHER INFORMATION: 10-347-348
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OTHER INFORMATION: 10-347-203
NAMES/KEY: 61161e
LOCATION: 6484
OTHER INFORMATION: 10-347-220
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LOCATION: 6534
OTHER INFORMATION: 10-347-271
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OTHER INFORMATION: 10-346-305
NAME/KEY: allele
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LOCATION: 5903
OTHER INFORMATION: 10-346-23
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LOCATION: 4062
OTHER INFORMATION:
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OTHER INFORMATION: 10-343-339
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LOCATION: 3802
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APPLICANT: Bougueleret, Lydie
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APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GEN
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACI
FILE REFERENCE: GEN-TIL14XCD1
CURRENT APPLICATION NUMBER: US/10/170,097
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/275,267
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-03-21
PRIOR FILING DATE: 1999-02-12
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US-10-170-097-651/c
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OTHER INFORMATION: 10-507-321
NAME/KBY: allele
LOCATION: 13524
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OTHER INFORMATION: 10-350-332 : polymorphic base C
NAME(KEY: allele
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SEQ ID NO 651
LENGTH: 206
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NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon 1
                                                              NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                             NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon
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LOCATION: 5996..6099
OTHER INFORMATION: exon
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ORGANISM: Homo sapiens
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LOCATION: 16567..16667
OTHER INFORMATION: exon
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LOCATION: 6349..6509
OTHER INFORMATION: exon
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LOCATION: 3871..4072
OTHER INFORMATION: exon
COCATION: 1128
OTHER INFORMATION: 10-508-191
                                  NAME/KEY: allele
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THER INFORMATION: exon 11
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JOCATION: 13308..13429
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OTHER INFORMATION: exon 10
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LOCATION: 8645..8854
OTHER INFORMATION: exon
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LOCATION: 7379..7522
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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LOCATION: 5758.
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LOCATION: 5552..5633
OTHER INFORMATION: exon
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FEATURE:
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION:
FEATURE:
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NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION:
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LOCATION: 1827
OTHER INFORMATION: 1
FEATURE:
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NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 2832
                                     NAME/KEY: allele
LOCATION: 5903
                                                                                                                                                                    NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 1182
OTHER INFORMATION:
                     LOCATION: 5903
OTHER INFORMATION:
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LOCATION: 3802
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LOCATION: 2844
OTHER INFORMATION:
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LOCATION: 2341
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LOCATION: 2048
OTHER INFORMATION:
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LOCATION: 2934
OTHER INFORMATION:
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LOCATION: 2623
OTHER INFORMATION:
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LOCATION: 2323
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OTHER INFORMATION:
NAME/KEY: allele
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LOCATION: 1570
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US-08-998-416-1036/c
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                                                                Sequence 1036, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
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Best Local Similarity
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NAME/KEY: allele
1777TON: 6141
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LOCATION: 6484
OTHER INFORMATION: 10-347-220
                  APPLICANT:
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LOCATION: 6467
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OTHER INFORMATION:
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LOCATION: 6375
OTHER INFORMATION:
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LOCATION: 6338
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LOCATION: 6183
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OTHER INFORMATION:
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OTHER INFORMAT
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        Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
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Pred. No. 0.038;
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Best Local Similarity 46.3%;
Matches 146; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/98,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Tinothy
REGISTRATION NUMBER: 38,241
RESPENSATE OF THE STANDARD RESPONSED TO THE S
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INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                         639 GATACTCTGCAAGCT
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DEDNESS: single
                                                      AATATTATGAAAGGT 418
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                           653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44.6; DB 3;
Pred. No. 0.01;
0; Mismatches 169;
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638 493 553 518 458 673 398

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US-10-104-047-682/c
; Sequence 682, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 fu.
; FILE REFERENCE: H1-A0105
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/10/104,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: promoter LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54;
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                                                                                                                                                                                                                             CSKWWNNYAAWYTKSSWNYTSRYYRWK 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGWDDDTKYHMWNNNGCBTVTWMVRYKTDRDWSBKRMNYGMBWWKNWSYDVTYYWWVWDD
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                                      6943241el full length cDNA
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Pred. No. 0.02;
27; Mismatches 215; Indels
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; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(80411)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-15777
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; Sequence 15777, Application US/09949016
; Patent No. 6812339
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                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15777
LENGTH: 80411
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SEQ ID NO 682
LENGTH: 2308
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                Local
17141 AAATGACATCTTTAATTCCTTATCCAAGCTAAAGTACATTTATGTATCATGATATGTTAT 1708:
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                               305 AACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTGTTAA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 TACCAACAAGACTTTACTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTT
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                                                                  Conservative
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3 OF DETECTION
                                                                                                 Length 80411;
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                                                              Gaps
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FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13272

LENGTH: 95020
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US-09-949-016-12063
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US-09-949-016-12063
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Best Local Similarity
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SOFTWARE: FRANKSEQ for Windows Version 4.0
SEQ ID NO 12063
LENGTH: 93493
                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12063, Appl Patent No. 6812339 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                            ACCTGCATAAATTCCTAAATGAATGTAACCCTGAACTTGCCTTATAAAGTTA 13518
                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTAATTTTATTCCTAAAAGAACAGAAACTTTCACTATGCTTTAAAAATTAA 625
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OF DETECTION
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US-09-662-254B-25
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US-09-949-016-13272
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GENERAL INFORMATION:
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Bawden, Alison Louise
TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
TITLE OF INVENTION: Vertebrate Cells
FILE REFERENCE: UP-221CIXCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/662,254B
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/086,651
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Amsacta moorei entomopoxvirus
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17406 TIGATAGTAATTATTTGTTTAGAGAATATAATAGATTATTA 17364
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                                   669 CAGACAGACAGAGCCCCCAGCTACTCTCTAGGAAATAATTA 711
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                                                                                                                                                                                                                                                           CTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTTACAATAAAG 548
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                                                                         CTGTAATTTTATTCCTAAAAGAACAGAAACTTTCACTATGCTTTAAAATTAA
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Pred. No. 0.69;
0; Mismatches 81;
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-83376
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US-09-949-016-83376/c
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; ORGANISM: Human
US-09-949-016-83375
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US-09-949-016-83375/c
                                                                          PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 83376
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Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 83376, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                         PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT FILING DATE: 2000-04-14
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                                                         LENGTH:
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Query Match

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SEQ ID NO 14143
LENGTH: 143550
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Best Local Similarity 51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                       100975 TAAGAAGTTAGAAA
                                                                                                                                         100915 TTTANATGCATATAATAAAGAAGATAAAATAATGCAAATTAAAAGCCTAAGCATTATTCT
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

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5: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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| 8  | d dd  | B &   | B 8  | B 8  | DB 09  | Que<br>Best<br>Mat   | RESUL' US-10.  Seq GENN GENN HI  |            |   |
| 301 ACTTAACAGACAATTAATCAGGCCAAACCACTTTAAGTTTTATTTGTATAGTATTTTGTG 3 | 241 GIGAAGGAAAAGGIGTATGTTTGCTCTCCGACATACTTCACTCAAATAICTATTGTT 3 | 181 TGGGACTAATTTAATCAGGAACATGCCACAGAGTGATGAGCCCGGAGGAAACCCTGATACA 2 | 121 ATGGCCAGGGGCTTTTGAACTTAATTAAAAGGGGAAAGTGATTTGCCTGAGCCCACTGAC 1 | 61 TGGACCAGAGCCACAGAGCTGGAAGTGTTTTAGAAGTCAGTGCAGCCCCCAGCTTTT : | 1 GAGTCTTCCCAGTACCGATCTCTGCAGCATTAACTTCTAGTCATGAAGGGGTGGTGACTC 6 | uery Match 100.0%; Score 1220; DB 7; Length 1220; est Local Similarity 100.0%; Pred. No. 2.4e-308; atches 1220; Conservative 0; Mismatches 0; Indels 0; Gaps | RESULT 1  IS-10-627-075-1  IS-10-627-075-1  Sequence 1, Application US/10627075  Publication No. US20040091913A1  GENERAL INFORMATION:  APPLICANT: Livingston et al.  TITLE OF INVERTION: Composition and Method for Imaging Cells  FILE REFERENCE: 20363-019  CURRENT APPLICATION NUMBER: US/10/627,075  CURRENT FILING DATE: 2003-07-24  PRIOR APPLICATION NUMBER: 60/398,583  PRIOR FILING DATE: 2002-07-25  NUMBER OF SEQ ID NOS: 1  SEQ ID NO 1  LENGTH: 1220  TYPE: DNA  ORGANISM: Mus musculus  IS-10-627-075-1 | ALIGNMENTS | 24 49 4.0 6127 6 US-10-240-485-2 Sequence 2, Appli 25 48.6 4.0 4687 3 US-09-918-995-5922 Sequence 1091, Ap 26 48.6 4.0 4687 3 US-09-918-995-5922 Sequence 93, Appl 27 48.4 4.0 2265 8 US-10-221-613-93 Sequence 33, Appl 28 48.2 4.0 2265 8 US-10-602-494-130 Sequence 37, Appl 29 48 3.9 5919 6 US-10-311-455-362 Sequence 17606, Appl 39 5919 7 US-10-221-613-64 Sequence 362, Appl 39 48 3.9 8056 8 US-10-473-126-386 Sequence 362, Appl 39 8056 8 US-10-473-126-386 Sequence 378, Appl 39 8058 8 US-10-473-126-386 Sequence 305, Appl 39 47.8 3.9 16724 6 US-10-311-455-1063 Sequence 279, Appl 39 47.6 3.9 16724 6 US-10-311-455-1063 Sequence 1063, Appl 39 47.6 3.9 1478 SUS-10-311-455-1063 Sequence 1079, Appl 47.6 3.9 6103 6 US-10-311-455-1664 Sequence 1079, Appl 47.6 3.9 6103 6 US-10-311-455-1664 Sequence 1079, Appl 47.6 3.9 8056 8 US-10-312-841-1 Sequence 1079, Appl 47.6 3.9 8056 8 US-10-312-841-1 Sequence 1079, Appl 47.6 3.9 8056 8 US-10-312-841-1 Sequence 1079, Appl 47.4 3.9 302 3 US-09-814-353-533 Sequence 1079, Appl 47.4 3.9 302 3 US-09-814-353-533 Sequence 1079, Appl 47.4 3.9 302 3 US-09-814-353-533 Sequence 1079, Appl 47.4 3.9 302 3 US-09-814-353-11622 Sequence 1079, Appl 47.4 3.9 302 3 US-09-814-353-533 Sequence 1079, Appl 54.5 47.2 3.9 2240 8 US-10-473-126-102 Sequence 1079, Appl 54.5 47.2 3.9 2240 8 US-10-473-126-102 Sequence 1079, Appl 54.5 47.2 3.9 2240 8 US-10-473-126-102 Sequence 1079, Appl 54.5 47.2 3.9 2240 8 US-10-473-126-102 Sequence 1079, Appl 54.5 47.2 3.9 2240 8 US-10-473-126-102 |
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RESULT 2
US-10-764-420-1571
Sequence 1571, Application US/10764420
Publication No. US20050084872A1
GENERAL INFORMATION:
APPLICANT: Lum, Pek Yee
APPLICANT: Tan, Yejun
APPLICANT: Dai, Hongyue
TITLE OF INVENTION: Methods For Determination of Invention of 
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  NAME/KEY: exon
LOCATION: 26810..26897
OTHER INFORMATION: exon
                                                                       NAME/KEY: exon
LOCATION: 10115..10233
OTHER INFORMATION: exon
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Sequence 1, Application US/09790289
Publication No. US20030165826A1
GENERAL INFORMATION:
APPLICANT: Caroline Barry
APPLICANT: Llya Chumakov
TITLE OF INVENTION: PG-3 and Biallelic Markers The FILE REFERENCE: 68 US3. REG
CURRENT APPLICATION NUMBER: US/09/790,289
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent.pm
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ROSA122057
CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR APPLICATION NUMBER: US 60/474,413
PRIOR APPLICATION NUMBER: US 60/474,413
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 3683
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1571
LENGTH: 2475
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-790-289-1/c
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1.2000
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 2001..2079
OTHER INFORMATION: exon A
NAME/KEY: exon
LOCATION: 4627..4718
OTHER INFORMATION: exon B
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Best Local Similarity 100.0%;
Matches 276; Conservative (
                                                                                                                                                                                                               LENGTH: 240825
TYPE: DNA
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LOCATION: 10286
OTHER INFORMATION: 5-392-280 : |
NAME/KEY: allele
LOCATION: 10370
OTHER INFORMATION: 5-392-364 : |
NAME/KEY: allele
LOCATION: 3994
OTHER INFORMATION: 4-58-318 : po
NAME/KEY: allele
LOCATION: 39973
OTHER INFORMATION: 4-58-289 : po
NAME/KEY: allele
LOCATION: 41385
OTHER INFORMATION: 4-54-199 : po
NAME/KEY: allele
LOCATION: 41404
OTHER INFORMATION: 4-54-180 : po
NAME/KEY: allele
LOCATION: 4232
OTHER INFORMATION: 4-54-180 : po
NAME/KEY: allele
LOCATION: 69521
OTHER INFORMATION: 99-86-266 : I
NAME/KEY: allele
LOCATION: 69521
OTHER INFORMATION: 4-88-107 : po
NAME/KEY: allele
LOCATION: 72838
OTHER INFORMATION: 5-397-141 : I
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LOCATION: 31357..31471
OTHER INFORMATION: exon E
NAME/KEY: exon
LOCATION: 34261..34404
OTHER INFORMATION: exon F
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LOCATION: 95111.95188
OTHER INFORMATION: exon J
NAME/KEY: exon
LOCATION: 216015..216252
OTHER INFORMATION: exon K
NAME/KEY: exon
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LOCATION: 37377...37466
OTHER INFORMATION: exon
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LOCATION: 4601
COTHER INFORMATION: 5-391-43 : polymorphic base A
NAME/KEY: allele
LOCATION: 10228
OTHER INFORMATION: 5-392-222 : polymorphic base G
OTHER INFORMATION: 5-392-222 : polymorphic base G
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 237526..238825
OTHER INFORMATION: exon L
NAME/KEY: misc feature
LOCATION: 238826..240825
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1999
LOCATION: 5-390-177 : polymorphic base G or C
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LOCATION: 39704..40858
OTHER INFORMATION: exon T
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LOCATION: 75989..76151
OTHER INFORMATION: exon I
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LOCATION: 72881..72918
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LOCATION: 50436..50545
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                    5-397-141 : polymorphic base G or T
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| TION: 1231 R INFORMAT /KEY: alle /ION: 1232 TION: 1232 R INFORMAT /KEY: alle /KEY: alle                                       | /KEY: alle<br>TION: 1220<br>R INFORMAT<br>/KEY: alle | Z La                                | OTHER INFORMATION  NAME/KEY: allele  LOCATION: 114604  OTHER INFORMATION | KEY<br>NON<br>NEW<br>NON                           | LOCATION OTHER INI NAME/KEY                         | LOCATION<br>OTHER IN                                | LOCATION<br>OTHER IN                        | NAME/KEY: LOCATION: OTHER INFO                          | LOCATION:<br>OTHER INFO | LOCATION: 1035<br>OTHER INFORMAT | LOCATION: 9896 OTHER INFORMAT | LOCATION: 9891<br>OTHER INFORMAT<br>NAME/KEY: alle | LOCATION: 9802<br>OTHER INFORMAT<br>NAME/KEY: alle   | OTHER INFORMAT NAME/KEY: alle                    | OTHER INFORMAT                                | OCATION: 9551 OTHER INFORMAT NAME/KEY: alle        | LOCATION: 9534<br>OTHER INFORMAT<br>NAME/KEY: alle | LOCATION: 9191<br>OTHER INFORMAT<br>NAME/KEY: alle     | LOCATION: 8392<br>OTHER INFORMAT<br>NAME/KEY: alle   | LOCATION: 8125<br>OTHER INFORMAT<br>NAME/KEY: alle     | ATION: 7606<br>ER INFORMAT<br>E/KEY: alle            |
|---|--|-------------------------------------|--|--|---|---|---|---|-------------------------|----------------------------------|-------------------------------|--|--|--|---|--|--|--|--|--|--|
| 24<br>24<br>10N: 99-12767-36 : polymorphic base G or C<br>1e<br>31<br>10N: 99-12767-143 : polymorphic base C or T<br>1e<br>1e | N: 99-78-321 : polyπ                                 | N: 4-84-334 : polymorphic base A or | : 4-44-277 : polym   | 72<br>10N: 4-45-49 : polymorphic base C or T<br>le | le<br>10N: 4-105-86 : polymorphic base A or G<br>le | 16<br>15<br>10N: 4-105-98 : polymorphic base A or G | 10N: 99-12758-136 : polymorphic base C or T | 16<br>73<br>10N: 99-12758-102 : polymorphic base A or G | : 99-12757-318 :        |                                  | – μ ω                         |  | 4<br>ION: 5-364-252 : polymorphic base G or T<br>.le | 10N: 99-12753-34 : polymorphic base A or T<br>le | TON: 4-23-326 : polymorphic base A or G<br>le | I<br>TON: 4-21-317 : polymorphic base G or T<br>le | 9<br>ION: 4-21-154 : polymorphic base C or T<br>le | 7<br>ION: 99-12749-175 : polymorphic base C or T<br>le | 1<br>ION: 99-109-358 : polymorphic base A or C<br>le | 3<br>ION: 99-12738-248 : polymorphic base A or C<br>le | 0<br>TON: 5-398-203 : polymorphic base A or C<br>.le |

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Query Match
Best Local Similarity
Matches 545; Conserv
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LOCATION: 128687
OTHER INFORMATION: 4-35-240 : polymorphic base G
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LOCATION: 128594
OTHER INFORMATION: 4-35-333
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LOCATION: 128333
OTHER INFORMATION: 4-36-261
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LOCATION: 128210
OTHER INFORMATION: 4-36-384
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LOCATION: 126738
OTHER INFORMATION: 4-80-328
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LOCATION: 128330
OTHER INFORMATION: 4-36-264
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NAME/KEY: allele
LOCATION: 123468
OTHER INFORMATION: 99-12767-380
                                               157974 TGGTTGGAGGGCAGGCATTCTGCTCTGATTTTTCCTGTTTGCCTGGCTAGTGACCCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                      158154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158512 AAATTCTAATTTCTCTATTGTAATGTAATGAACTTAATCAGTACAGTGTATTTTTAGAGT 158453
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                                                                                                                                                                                               CATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCAGAAGGCTTCTGCAGTACACAGTC
                                                                                                                                                                                                                                                                TCAGACAAAAGAGATCAACTGCTCTCTAGGAAATACTTAATTGGGGTGGTGCCTAGGA
AGGAAGATAGTGGGTGAGCCAGG-GGGCGGAGCGGCTGGCTGCACATGTCTGGCTGCTCT
                                                                                    CTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTAC
                                                                                                                                                                                                                                                                                                          ACAGACAACAGAGCCCCA-GCTACTCTCTAGGAAA----TAATTAGGGTGCTGCCTCTGA 726
                                                                                                                                                                                                                                                                                                                                                                     CTTCAACATTAAAGTTATTACCTCAGATATTTTGCCAGCTTAGCACGGCAAAAATCAGTT 158095
                                                                                                                                                                                                                                                                                                                                                                                                               CTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTAGCCTACAAACGAGCAG-- 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTÉCTGACCTATTTGTAGTATTTTTATTCCTAAAGGAAAAAACAGGAACTTTCATTGTA 158155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTCCCGATATAGCTGTAATTTTATTCCTA-----AAAGAACAGAAACTTTCACTATG
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Pred. No. 4.7e-50;
0; Mismatches 265; Indels
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PUDILCATION NO. US20040163137A1
GENERAL INFORMATION:
APPLICANT: Genset
TITLE OF INVENTION: PG-3 and biallelic markers the FILE REFERENCE: 68.W02
CURRENT APPLICATION UNWBER: US/10/468,582
CURRENT FILING DATE: 2003-08-20
NUMBER OF SEQ ID NOS: 5
SOPTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 240825
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US-10-468-582-1/c
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LOCATION: 39704..40858
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LOCATION: 50436..50545
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LOCATION: 37377..37466
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LOCATION: 31357..31471
OTHER INFORMATION: exon
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LOCATION: 1..2000
OTHER INFORMATION: 5'regulatory region
                OTHER INFORMATION: exon
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OTHER INFORMATION:
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LOCATION: 26810.
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LOCATION: 10115..10233
OTHER INFORMATION: exon
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NAME/KEY: exon
LOCATION: 4627..4718
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LOCATION: 2001..2079
OTHER INFORMATION: exon
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ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: allele
LOCATION: 69521
OTHER INFORMATION: 4
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LOCATION: 41385
OTHER INFORMATION: 4
FEATURE:
NAME/KEY: allele
LOCATION: 41404
OTHER INFORMATION: 4
FEATURE:
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NAME/KEY: allele
LOCATION: 39973
COTHER INFORMATION: 4
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NAME/KEY: allele
LOCATION: 10370
OTHER INFORMATION: 5
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NAME/KEY: allele
LOCATION: 10228
OTHER INFORMATION: 5
FEATURE:
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NAME/KEY: allele
LOCATION: 39944
OTHER INFORMATION: 4
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LOCATION: 238826..240825
OTHER INFORMATION: 3'regulatory region
FEATURE:
NAME/KEY: allele
LOCATION: 1999
OTHER INFORMATION: 5-390-177 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 4601
FEATURE:
NAME/KEY: allele
                                                                                NAME/KEY: allele
LOCATION: 67475
OTHER INFORMATION:
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NAME/KEY: exon
LOCATION: 95111..95188
OTHER INFORMATION: exon J
                                                                                                                                      NAME/KEY: allele
LOCATION: 42232
OTHER INFORMATION:
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NAME/KEY: exon
LOCATION: 216015..216252
OTHER INFORMATION: exon K
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LOCATION: 72881..72918
OTHER INFORMATION: exon
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LOCATION: 10286
OTHER INFORMATION:
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OTHER INFORMATION: 5-391-43
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LOCATION: 237526..238825
OTHER INFORMATION: exon L
FEATURE:
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LOCATION: 75989..76151
OTHER INFORMATION: exon
                     4-88-107 : polymorphic base A or
                                                                                99-86-266
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| NAME/KEY: allele | NAME/KEY: allele<br>LOCATION: 108327<br>OTHER INFORMATION: 4-1 | Y: allele<br>N: 108315<br>NFORMATION: 4- | NAME/KEY: allele LOCATION: 106407 OTHER INFORMATION: 99 | : allele<br>: 106373<br>FORMATION: 99 | : allele<br>: 104398<br>:FORMATION: 99 | : allele<br>: 103593<br>FORMATION: 4- | : allele<br>: 98963<br> FORMATION: 99 | NAME/KE: allele LOCATION: 98914 OTHER INFORMATION: 99 | : allele<br>: 98024<br>FORMATION: 5- | NAME/KEY: allele LOCATION: 97294 OTHER INFORMATION: 99 | : allele<br>1: 96190<br>FORMATION: 4- | : allele<br>1: 95511<br>FORMATION: 4- | : allele<br>1: 95349<br>FORMATION: 4- | Y: allele<br>N: 91917<br>NFORMATION: 99 | NAME/KEY: allele<br>LOCATION: 83921<br>OTHER INFORMATION: 99 | f: allele<br>7: 81253<br>FORMATION: 99 | NAME/KEY: allele LOCATION: 76060 OTHER INFORMATION: 5- | 1: 72838<br>FORMATION: 5- |
|                  | 105-86 :   | 105-98 :                                 | -12758-136  | -12758-102                            | -12757-318                             | 87-212 :                              | -12755-329                            | -12755-280  | 364-252 :                            | -12753-34  | 23-326 :                              | 21-317 :                              | 21-154 :                              | -12749-175                              | -109-358   | -12738-248                             | 398-203 :  | 397-141 :                 |
|                  | polymorphic base A or G  | polymorphic base A or G                  | : polymorphic base C or T                               | : polymorphic base A or G             | : polymorphic base C or T              | polymorphic base A or G               | : polymorphic base A or C             | : polymorphic base A or G                             | polymorphic base G or T              | : polymorphic base A or T                              | polymorphic base A or G               | polymorphic base G or T               | polymorphic base C or T               | : polymorphic base C or T               | : polymorphic base A or C                                    | 3 : polymorphic base A or C            | polymorphic base A or C                                | polymorphic base G or T   |

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RESULT 5
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   Sequence 1, Application US/11028971
Publication No. US20050158779A1
GENERAL INFORMATION:
APPLICANT: Caroline Barry
APPLICANT: 11ya Chumakov
TITLE OF INVENTION: PG-3 and Biall
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19.5%; Score 238; DB 7; Length 240825;
Best Local Similarity 64.3%; Pred. No. 4.7e-50;
Matches 545; Conservative 0; Mismatches 265; Indels 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTGTTGCCTGGCTAGTGACCCCCTAC
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and Biallelic Markers
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FILE REFERENCE: 68.US3.REG
CURRENT APPLICATION NUMBER: US/11/028,971
CURRENT FILING DATE: 2005-01-04
PRIOR APPLICATION NUMBER: US/99/790,289
PRIOR FILING DATE: 2001-02-23
INUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 240825
TYPE: DNA
                                                                                                                                                                                                                      FEATURE:
NAME/KEY: exon
NAME/KEY: 75989.
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                               FEATURE:
NAME/KEY: exon
LOCATION: 237526..238825
OTHER INFORMATION: exon
                                                                                         NAME/KEY: exon
LOCATION: 216015..2
OTHER INFORMATION:
                                                                                                                                                    LOCATION: 95111..95
OTHER INFORMATION:
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LOCATION: 95111..95188
NAME/KEY: misc_feature
                                                                                                                                                                                                            LOCATION: 75989..76
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 72881..72918
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LOCATION: 39704..40858
OTHER INFORMATION: exon
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LOCATION:
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LOCATION: 31357..31471
THEOREMATION: exon
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LOCATION: 50436..50545
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LOCATION: 26810..26897
OTHER INFORMATION: exo
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LOCATION: 2001..2079
OTHER INFORMATION: e:
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OTHER INFORMATION: exon
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LOCATION: 34261..34
OTHER INFORMATION:
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LOCATION: 10115...10233
OTHER INFORMATION: exon
FEATURE:
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LOCATION: 4627..4718
OTHER INFORMATION: exon
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OTHER INFORMATION: 5'regulatory region
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PEATURE:
NAME/KEY: allele
NAME/TON: 76060
                             LOCATION: 91917
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 69521
OTHER INFORMATION:
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LOCATION: 39973
OTHER INFORMATION:
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OTHER INFORMATION:
                                           NAME/KEY: allele LOCATION: 91917
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OTHER INFORMATION:
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LOCATION: 67475
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 10370
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 81253
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LOCATION: 72838
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LOCATION: 41385
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LOCATION: 39944
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OTHER INFORMATION: 3'regulatory
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Best Local Similarity 64.3
Matches 545; Conservative
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LOCATION: 103593
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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LOCATION: 106407
OTHER INFORMATION:
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LOCATION: 98963
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LOCATION: 98914
OTHER INFORMATION:
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LOCATION: 98024
OTHER INFORMATION:
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LOCATION: 97294
OTHER INFORMATION:
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LOCATION: 95511
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LOCATION: 108327
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LOCATION: 104398
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LOCATION: 96190
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ACTTGGCTAGTGGTTCAAGAATCAACTAAAATCAATGAATCTATTTTTCCCTCTGAAAAG 158275
                       AATGTGCATAACTTAAAAAAAAAACCAAATACCAACAAGACTTTACTTCCCCTTGGAAAA
                                                CTAACGTGACTTAATAACAGATCTTTCTATCCAACTGTTCGGAAATGAAAAATCTTTTGTA 158335
                                                                          GTAACTTGATTTAATAA-----
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Pred. No. 4.7e-50;
0; Mismatches 265;
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF ANGIOPOIETIN-2 EXPRESSION
FILE REFERENCE: RTS-0454
CURRENT APPLICATION NUMBER: US/10/317,803
CURRENT FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 244
SEQ ID NO 11
LENGTH: 2424
TYPE: DNA
ORGANISM: M. musculus
PPATTIDE: DNA
ORGANISM: M. musculus
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                                                                                                   Query Match
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NAME/KEY: misc_feature
LOCATION: 2308
OTHER INFORMATION: n = A, T, C
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NAME/KEY: CDS
LOCATION: (211)...(1701)
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                                                            h 17.5%; Score 213; DB 7; L Similarity 100.0%; Pred. No. 1.3e-44; 13; Conservative 0; Mismatches 0;
AAGTGAGC 157727
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                                                                                             Length 2424;
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RESULT 8
US-10-827-759A-5
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; NAME/KEY: misc feature
; LOCATION: (2308)..(2308)
; OTHER INFORMATION: n is a,
US-10-789-222-34
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US-10-789-222-34
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                                                                                                                                                      Sequence 5, Application US/10827759A Publication No. US20040248174A1 GENERAL INFORMATION:
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APPLICANT: The Trustees of the University of Pennsylvania APPLICANT: Samuel Jotham Reich APPLICANT: Samuel Jotham Reich APPLICANT: Michael J. Tolentino TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SIRNA TITLE OF INVENTION: INHIBITION OF ANGIOPOIETIN 1 AND 2 AN FILE REFERENCE: 43826-0005 US1
CURRENT APPLICATION NUMBER: US/10/827,759A
CURRENT FILING DATE: 2004-04-19
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Best Local S
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Publication No. US20040186054A1
GENERAL INFORMATION:
APPLICANT: Yu, Qin
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es 213; Conserv
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; PRIOR APPLICATION NUMBER: US 60/463,981
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2424
; TYPE: DNA
; ORGANISM: Mus musculus
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US-10-317-803-4
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10317803
Publication No. US20040115640A1
GENERAL INFORMATION:
APPLICANT: Kathleen Myers
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF ANGIOPOIETIN-2 EXPRESSION
FILE REFERENCE: RTS-0454
CURRENT APPLICATION NUMBER: US/10/317,803
CURRENT FILING DATE: 2002-12-11
                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4
LENGTH: 62705
TYPE: DNA
ORGANISM: H. sapiens
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Best Local Similarity
Matches 213; Conserv
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Best Local Similarity
Matches 335; Conserv
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NAME/KEY: misc_feature
LOCATION: 2308
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                  GAAGGCTTCTGCAGTACACAGTCCTTTGGGGCAGTAAGCACTATGCTCTGATTTTTCCTG
                                                         CTTAATTGGGGTGCTGCCTAGGAAATGCCCAGGGTCCTGTAACAGATCGGTTTTTCCCA
                                                                           ---TAATTAGGGTGGTGCCTCTGACATGCCCAGGGGTCTTGTGGCTGGTCTG-TGTTCCCA
GCTTAGCACGGCAAAAATCAGTTTCAGACAAAAGAGATCAACTGCTCTCTAGGAAATA 150
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Pred. No. 1.3e-44;
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GENERAL IMPORMATION:
APPLICANT: Olga Bandman
ITITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 24
LENGTH: 3251
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                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyt
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                                                TTTTCCTGTTGCCTGGCTAGTGACCCCCTACAGGAAGATAACGGCTAAGCCAGGAGGGCG
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Pred. No. 8.9e-30;
0; Mismatches 69
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US-10-433-793-187
; Sequence 187, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angio
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/433,793

Diagnose von mit Angiogenese

assoziierten

Krankheiten

RESULT 11

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US-10-433-793-188/c
                                                                                                                            ; OTHER INFORMATION: US-10-433-793-188
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                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 188
LENGTH: 2846
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                         Sequence 188, Application US/10433793
Publication No. US20040142334A1
GENERAL INFORMATION:
                                                                                 Query Match
Best Local
                                                                     Matches
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Best Local Similarity
Matches 295; Conserv
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NUMBER OF SEQ ID NOS:
SEQ ID NO 187
LENGTH: 2846
                                                                                                                                                                                                                                                               APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von mit Angiogenese
FILE REFERENCE:
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ORGANISM: Artificial
FEATURE:
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                                                                  Conservative
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                                                                                                                                    chemically treated genomic DNA
                                                                            11.48;
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                                                                Score 139.4; I
Pred. No. 2.6e
0; Mismatches
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Pred. No. 1.3e-25;
0; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic DNA (Homo sapiens)
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APPLICATION NUMBER: DCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DCT/EP01/07537
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DCT/EP01/07537
PRIOR FILING DATE: 2000-09-01
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Publication No. US20030143606A1
GENERAL INFORMATION:
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Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
                                                                                                                                                                                                           SEQ ID NO 2114
LENGTH: 15698
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Best Local :
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SEQ ID NO 866
LENGTH: 10710
TYPE: DNA
                                                                                                                                -10-311-455-2114
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014 CURRENT APPLICATION NUMBER: US/10/311,455 CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                            OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens
                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                               TYPE: DNA
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TTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTACAATAAAGAAAATAA
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Pred. No. 0.0067;
0; Mismatches 155;
                                                           Score 54.4; DB 6;
Pred. No. 0.012;
0; Mismatches 121;
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Search completed: December 12, Job time: 1003 secs

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US-10-602-494-272
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APPLICANT: Andrew Sledziewski
APPLICANT: Jeff Thomas
APPLICANT: Robert W. Day
APPLICANT: Lori Tonnes-Priddy
APPLICANT: Karen Cardon
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SEQ ID NO 272
LENGTH: 2265
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Best Local Similarity 52.5%;
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TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-45
CURRENT APPLICATION NUMBER: US/10/602,494
CURRENT FILING DATE: 2003-06-23
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7131 CACTACAA 7124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7251 AAATATCACTAAAAAATTAAAACAAAAAAAATAACATAATCTAAATTTCAATCTTAAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602
                                                                  542 AATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCTAAAAGAACAGAA
                                                                                                                                    482 GACTTTACTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTTTATATTTAC
                                                                                                                                                                                                                                       656 GCCTACAA 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596 ACAGAAACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGATACTCTGCAAGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 CAACAAGACTTTACTTCCCCTTGGAAAAGCACATTTACAAGGGCTGATCTTAGCCTTTAT
42
                                                                                                                                                                                                      ACTTTCACTATGCTTTAAAATTAAAGTGATTACCTCAGA
ACTAACACAATACAAATACCCTAAACACACTAAATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTCTAACTAACAACAAAATAAAAAAAAAACACGACAAAAACCAAAAAACCAATTAAAAAAAC 7132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTACAATAAAGAAAATAAACCAAGGTCCCGATATAGCTGTAATTTTATTCCTAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10602494
o. US20040265833A1
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                        Score 52.6; DB 8;
Pred. No. 0.012;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                           104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the analysis of colorectal cell
                                                                                                                                                                                                                                                                                                        Length 2265;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                         Gaps
                                                                                                   601
                                                                                                                                                                     541
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                                                                  43
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